May 2013

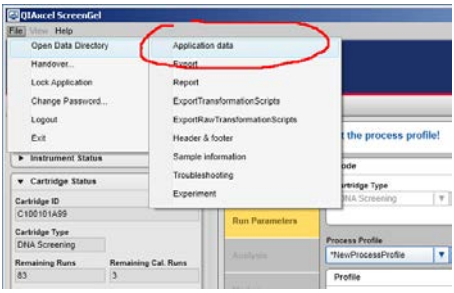
Important Note

Dear QIAxcel user,

Some users may encounter an unexpected error after updating their QIAxcel® ScreenGel® Software to the new version 1.2.0, if software version 1.0.x has been previously installed. To prevent this from occurring, several method files which are now obsolete must be manually removed from the method directory before using the software.

Follow the instructions below to remove these method files. Refer to the *QIAxcel Advanced User Manual* for more information.

1. **Install and start QIAxcel ScreenGel Software version 1.2.0.**
2. **Navigate to the parent method directory using the menu command "Open Data Directory/Application data" provided in QIAxcel ScreenGel Software. The default location is C:\ProgramData\QIAGEN\QIAxcel\ScreenGel\Data\Method for Microsoft Windows 7 or C:\Documents and Settings\All Users\Application Data\QIAGEN\QIAxcel\ScreenGel\Data\Method for Microsoft Windows XP Professional.**



QIAGEN®

Sample & Assay Technologies

3. **Delete the following 6 method files from the list:**
   BH1200.xmt
   BH800.xmt
   BL1200.xmt
   BL800.xmt
   BM1200.xmt
   BM800.xmt
4. **The software is now ready for use.**

If you have any issues running the QIAxcel ScreenGel Software, please contact QIAGEN.

Best regards,

QIAGEN

Trademarks: QIAGEN®, QIAxcel®, ScreenGel® (QIAGEN Group).

March 2013

QIAxcel® Advanced User Manual

For use with QIAxcel ScreenGel® Software v1.2

QIAGEN®

Sample & Assay Technologies

Trademarks

QIAGEN®, QIAsymphony®, QIAxcel®, ScreenGel® (QIAGEN Group); Adobe®, Reader® (Adobe Systems Inc.); Excel®, Microsoft®, Windows® (Microsoft Corporation); Intel®, Celeron® (Intel Corporation).

Registered names, trademarks, etc. used in this document, even when not specifically marked as such, are not to be considered unprotected by law.

© 2012–2013 QIAGEN, all rights reserved.

Contents

1 Safety Information 1-2

1.1 Proper use ... 1-2
1.2 Electrical safety ... 1-3
1.3 Environment ... 1-4
1.4 Chemicals ... 1-4
1.5 Waste disposal ... 1-5
1.6 Mechanical hazards ... 1-5
1.7 Symbols on the QIAxcel Advanced ... 1-5

2 Introduction 2-2

2.1 About this user manual ... 2-2
2.2 General information ... 2-2
2.3 Intended use of the QIAxcel Advanced ... 2-3
2.3.1 Requirements for QIAxcel Advanced users ... 2-4

3 General Description 3-2

3.1 QIAxcel Advanced principle ... 3-2
3.2 External features of the QIAxcel Advanced ... 3-3
3.3 Gel cartridges ... 3-4
3.4 Computer and software ... 3-5

4 Installation Procedures 4-2

4.1 Requirements ... 4-2
4.1.1 Site ... 4-2
4.1.2 Power requirements ... 4-2
4.1.3 Grounding requirements ... 4-3
4.2 Unpacking the QIAxcel Advanced ... 4-3
4.3 Installing the QIAxcel Advanced ... 4-3
4.3.1 Releasing the transport lock ... 4-4
4.3.2 Instrument setup ... 4-4
4.3.3 Installation of AC power cord ... 4-4
4.3.4 Installation of the N2 cylinder ... 4-5
4.3.5 Installation of the QIAxcel ScreenGel software ... 4-5
4.3.6 Getting started with the QIAxcel ScreenGel software ... 4-6
4.4 Packing the QIAxcel Advanced ... 4-6

5 Operating Procedures 5-2

5.1 Unpacking a QIAxcel Kit ... 5-2
5.2 Setting up the QIAxcel Advanced ... 5-3

5.2.1 Preparing the buffer tray ... 5-3
5.2.2 Loading the buffer tray ... 5-5
5.2.3 Installing a QIAxcel gel cartridge and smart key ... 5-5
5.2.4 Removing a QIAxcel gel cartridge ... 5-7
5.2.5 Storing a QIAxcel gel cartridge ... 5-7
5.3 Operating the QIAxcel Advanced ... 5-8
5.3.1 Things to do before starting ... 5-9
5.3.2 Starting a run ... 5-9
6 QIAxcel ScreenGel Software 6-2
6.1 Concepts ... 6-2
6.1.1 Modes ... 6-2
6.1.2 User roles ... 6-3
6.1.3 Environments ... 6-5
6.1.4 Profiles ... 6-5
6.1.5 General software usage ... 6-6
Editing data in tables ... 6-8
Displaying errors and warnings ... 6-9
Displaying modifications ... 6-11
Getting help ... 6-14
6.2 User authentication ... 6-15
6.3 Process ... 6-19
6.3.1 Running a process with advanced options ... 6-20
Provide Sample Information ... 6-27
6.3.2 Modifying a process profile ... 6-31
6.3.3 Process profile options ... 6-33
Selecting general process options ... 6-35
Selecting run parameters ... 6-36
Selecting analysis parameters ... 6-39
Selecting marker ... 6-41
Selecting peak calling instructions ... 6-43
Selecting report/export parameters ... 6-44
Run parameters and result structure ... 6-45
6.3.4 Creating a new process profile ... 6-49
6.3.5 Viewing method details ... 6-50
6.3.6 "Status Information" panel ... 6-51
6.4 Analysis ... 6-54
6.4.1 Handling samples and experiments ... 6-55
Meaning of sample icons ... 6-57
Loading sample data ... 6-57
Selecting samples ... 6-59
Selecting samples for analysis or report ... 6-60
Expanding and collapsing ... 6-61
Activating an experiment ... 6-61
Saving an experiment ... 6-62
Closing an experiment ... 6-64
Importing BioCalculator Data ... 6-64
Revising sample information ... 6-66
Handling an incomplete experiment ... 6-66
6.4.2 Viewing sample data ... 6-67
Adding samples to views ... 6-67
Removing samples from views ... 6-70

Exporting view to clipboard ... 6-72
Direct printing view ... 6-74
Result table ... 6-74
Gel view ... 6-79
Electropherogram view ... 6-83
Electropherogram overview ... 6-89
Electropherogram superposition view ... 6-92
Inspecting sample properties ... 6-95
Saturated signals ... 6-96
6.4.3 Peak detection ... 6-97
Peak detection procedure ... 6-98
Modifying an analysis profile ... 6-101
Creating a new analysis profile ... 6-106
6.4.4 Size and concentration determination ... 6-106
Size and concentration determination procedure ... 6-108
Creating a reference marker ... 6-110
Creating a new size marker table ... 6-113
6.4.5 Peak Calling ... 6-115
Modifying a peak calling instruction ... 6-117
Creating a new peak calling instruction ... 6-120
6.4.6 Analysis of DNA samples ... 6-121
6.4.7 Analysis of RNA samples ... 6-123
6.4.8 Analysis of protein samples ... 6-126
6.4.9 Manually modifying analysis results ... 6-131
Modifying the threshold ... 6-131
Deleting a peak ... 6-132
Adding a peak ... 6-132
Removing analysis results ... 6-133
Checking alignment marker ... 6-134
6.4.10 Customizing experiments ... 6-134
Creating a new experiment ... 6-135
Modifying an experiment ... 6-135
6.4.11 Report/Export ... 6-138
Generating a report ... 6-139
Report options ... 6-140
Exporting data ... 6-154
Export options ... 6-155
Modifying a report/export profile ... 6-163
Creating a new report/export profile ... 6-164
6.5 Service ... 6-165
6.5.1 Calibrating a cartridge ... 6-166
Running the calibration wizard ... 6-166
Recalibrating a cartridge ... 6-167
6.5.2 System Check ... 6-168
Complete Check ... 6-168
Detector Test ... 6-169
Filter Check ... 6-170
Movement Check ... 6-171
Leakage Test ... 6-172
6.5.3 Maintenance ... 6-172
Purge ... 6-173
Long purge ... 6-173
Empty N2 bottle ... 6-174
Setting the instrument ID ... 6-174

Troubleshooting folder and log files ... 6-175
6.6 Configuration ... 6-177
6.6.1 Settings ... 6-177
6.6.2 Profile management ... 6-182
6.6.3 User management ... 6-183
7 Maintenance Procedures 7-2
7.1 Cleaning of the QIAxcel Advanced ... 7-2
7.2 Minor corrective maintenance ... 7-3
7.2.1 Fuse replacement and cleaning ... 7-3
7.2.2 N2 cylinder replacement ... 7-3
7.2.3 Alternate N2 supply ... 7-4
7.2.4 Blocked purge filter ... 7-4
8 Troubleshooting 8-2
8.1 System setup ... 8-2
8.2 Operation ... 8-3
8.3 DNA applications ... 8-4
8.4 RNA applications ... 8-7
8.5 Protein applications ... 8-9
9 Glossary 9-2
10 Appendices 10-2
10.1 Appendix A ... 10-3
10.2 Appendix B ... 10-7
10.3 Appendix C ... 10-14
10.4 Appendix D ... 10-18
10.5 Appendix E ... 10-22
10.6 Appendix F ... 10-23
10.7 Appendix G ... 10-28
10.8 Appendix H ... 10-33

1. Safety Information

1 Safety Information

Before using the QIAxcel Advanced, it is essential that you read this user manual carefully and pay particular attention to the safety information. The instructions and safety information in the user manual must be followed to ensure safe operation of the instrument and to maintain the instrument in a safe condition.

The following types of safety information appear throughout this manual.

WARNING	The term WARNING is used to inform you about situations that could result in **personal injury** to you or other persons. Details about these circumstances are given in a box like this one.

CAUTION	The term CAUTION is used to inform you about situations that could result in **damage to the instrument** or other equipment. Details about these circumstances are given in a box like this one.

The advice given in this manual is intended to supplement, not supersede, the normal safety requirements prevailing in the user's country.

1.1 Proper use

WARNING/ CAUTION	**Risk of personal injury and material damage** **[W1]** Improper use of the QIAxcel Advanced may cause personal injuries or damage to the instrument. The QIAxcel Advanced must only be operated by qualified personnel who have been appropriately trained. Servicing of the QIAxcel Advanced must only be performed by QIAGEN Field Service Specialists.

Perform the maintenance as described in the Maintenance Procedures section. QIAGEN charges for repairs that are required due to incorrect maintenance.

WARNING/ CAUTION	**Risk of personal injury and material damage** **[W2]** The QIAxcel Advanced is too heavy to be lifted by one person. To avoid personal injury or damage to the instrument, do not lift the instrument alone.

WARNING/ CAUTION	**Risk of personal injury and material damage** **[W3]** Do not attempt to move the QIAxcel Advanced during operation.

CAUTION	**Damage to the instrument** **[C1]** Avoid spilling water or chemicals onto the QIAxcel Advanced. Damage caused by water or chemical spillage will void your warranty.

In case of emergency, switch off the QIAxcel Advanced at the power switch at the rear of the instrument and unplug the power cord from the power outlet.

CAUTION	**Damage to the instrument** [C2] If the "Pressure 1" status is "Low", increase system pressure before performing the "unlatch" command. Removing the cartridge and unlatching with reduced pressure may damage the instrument.

1.2 Electrical safety

Disconnect the line power cord from the power outlet before servicing.

WARNING	**Electrical hazard** [W4] Any interruption of the protective conductor (earth/ground lead) inside or outside the instrument or disconnection of the protective conductor terminal is likely to make the instrument dangerous. Intentional interruption is prohibited. **Lethal voltages inside the instrument** When the instrument is connected to line power, terminals may be live, and opening covers or removing parts is likely to expose live parts.

To ensure satisfactory and safe operation of the QIAxcel Advanced, follow the advice below:

- The line power cord must be connected to a line power outlet that has a protective conductor (earth/ground).
- Do not adjust or replace internal parts of the instrument.
- Do not operate the instrument with any covers or parts removed.
- If liquid has spilled inside the instrument, switch off the instrument, disconnect it from the power outlet, and contact QIAGEN Technical Services.
- When replacing the main fuse, replace only with the type and current rating specified on the rating label.

If the instrument becomes electrically unsafe, prevent other personnel from operating it, and contact QIAGEN Technical Services; the instrument may be electrically unsafe when:

- The line power cord appears to be damaged.
- It has been stored under unfavorable conditions for a prolonged period.
- It has been subjected to severe transport stresses.

1.3 Environment

Operating conditions

WARNING	**Explosive atmosphere** [W5] The QIAxcel Advanced is not designed for use in an explosive atmosphere.

WARNING	**Risk of explosion** [W6] The QIAxcel Advanced is intended for use with reagents and substances supplied with QIAGEN QIAxcel Kits. Use of other reagents and substances may lead to fire or explosion.

CAUTION	**Damage to the instrument** [C3] Direct sunlight may bleach parts of the instrument and cause damage to plastic parts. The QIAxcel Advanced must be located out of direct sunlight.

CAUTION	**Damage to the cartridge** [C4] When in use, the gel cartridge should not be left out of the "Wash park" position of the buffer tray for more than 15 minutes. Failure to do so will cause the capillary tips to dry out, affecting correct function of the cartridge. Dry tips will void the warranty. The capillary tips are made of glass and are very fragile. Take care not to knock the tips on any hard surfaces. Failure to do so will cause the capillary tips to break, affecting correct function of the cartridge. Broken tips will void the warranty.

1.4 Chemicals

WARNING	**Hazardous chemicals** [W7] Some chemicals used with this instrument may be hazardous or may become hazardous after completion of the run. Always wear safety glasses, gloves, and a lab coat. The responsible body (e.g., laboratory manager) must take the necessary precautions to ensure that the surrounding workplace is safe and that the instrument operators are not exposed to hazardous levels of toxic substances (chemical or biological) as defined in the applicable Safety Data Sheets (SDSs) or OSHA,* ACGIH,† or COSHH‡ documents. Venting for fumes and disposal of wastes must be in accordance with all national, state, and local health and safety regulations and laws.

* OSHA: Occupational Safety and Health Administration (United States of America).
† ACGIH: American Conference of Government Industrial Hygienists (United States of America).
‡ COSHH: Control of Substances Hazardous to Health (United Kingdom).

WARNING	**Risk of fire** [W8] When cleaning the QIAxcel Advanced with alcohol-based disinfectant, leave the QIAxcel Advanced doors open to allow flammable vapors to disperse.

1.5 Waste disposal

Used labware and containers may contain hazardous chemicals. Such wastes must be collected and disposed of properly according to local safety regulations.

For information about how to dispose of the QIAxcel Advanced, see Appendix A.

1.6 Mechanical hazards

The cartridge door and sample door of the QIAxcel Advanced must remain closed during operation of the instrument.

WARNING	**Moving parts** [W9] To avoid contact with moving parts during operation of the QIAxcel Advanced, the instrument must be operated with the cartridge door and sample door closed. If the door sensors are not functioning correctly, contact QIAGEN Technical Services.

1.7 Symbols on the QIAxcel Advanced

Symbol	Location	Description
	Type plate on the back of the instrument	CE mark
	Type plate on the back of the instrument	CSA listing mark for Canada and the USA
	Type plate on the back of the instrument	Legal manufacturer
	Type plate on the back of the instrument	Waste Electrical and Electronic Equipment (WEEE)
	Type plate on the back of the instrument	FCC mark of the United States Federal Communications Commission

This page intentionally left blank

2. Introduction

2 Introduction

Thank you for choosing the QIAxcel Advanced. We are confident it will become an integral part of your laboratory.

Before using the QIAxcel Advanced, it is essential that you read this user manual carefully and pay particular attention to the safety information. The instructions and safety information in the user manual must be followed to ensure safe operation of the instrument and to maintain the instrument in a safe condition.

2.1 About this user manual

This user manual provides information about the QIAxcel Advanced in the following sections:

- Safety Information
- Introduction
- General Description
- Installation Procedures
- Operating Procedures
- QIAxcel ScreenGel Software
- Maintenance Procedures
- Troubleshooting
- Glossary
- Appendices

The appendices include the following:

- Technical data
- QIAxcel Advanced methods and accessories
- Data analysis algorithm descriptions
- Warranty liability clause

2.2 General information

Technical assistance

At QIAGEN, we pride ourselves on the quality and availability of our technical support. Our Technical Services Departments are staffed by experienced scientists with extensive practical and theoretical expertise in sample and assay technologies and the use of QIAGEN® products. If you have any questions or experience any difficulties regarding the QIAxcel Advanced or QIAGEN products in general, do not hesitate to contact us.

QIAGEN customers are a major source of information regarding advanced or specialized uses of our products. This information is helpful to other scientists as well as to the researchers at QIAGEN. We therefore encourage you to contact us if you have any suggestions about product performance or new applications and techniques.

For technical assistance and more information, please see our Technical Support Center at www.qiagen.com/goto/TechSupportCenter or call one of the QIAGEN Technical Service Departments or local distributors (see back cover or visit www.qiagen.com).

Policy statement

It is the policy of QIAGEN to improve products as new techniques and components become available. QIAGEN reserves the right to change specifications at any time.

In an effort to produce useful and appropriate documentation, we would appreciate your comments on this user manual. Please contact QIAGEN Technical Services.

Version management

This document is the QIAxcel Advanced User Manual, version 3.0.

2.3 Intended use of the QIAxcel Advanced

The QIAxcel Advanced is a multicapillary electrophoresis instrument, designed to perform fast and fully automated DNA fragment analysis, qualitative and quantitative RNA analysis, or protein size and concentration analysis.

The QIAxcel Advanced instrument is intended to be used only in combination with QIAxcel Kits for applications described in the respective QIAxcel Kit handbooks.

The QIAxcel Advanced instrument is intended for use by professional users, such as technicians and physicians trained in molecular biological techniques and the operation of the QIAxcel Advanced instrument.

2.3.1 Requirements for QIAxcel Advanced users

This table covers the general level of competence and training necessary for transportation, installation, use, maintenance, and servicing of the QIAxcel Advanced.

Task	Personnel	Training and experience
Transportation	No special requirements	No special requirements
Installation	Laboratory technicians or equivalent	Appropriately trained and experienced personnel familiar with use of computers and automation in general
Instrument administration	Laboratory technicians or equivalent	Appropriately trained and experienced personnel familiar with use of computers and automation in general
Routine use (running profiles)	Laboratory technicians or equivalent	Appropriately trained and experienced personnel familiar with use of computers and automation in general
Analyzing data	Laboratory technicians or equivalent	Appropriately trained and experienced personnel familiar with use of computers and automation in general
Instrument maintenance	Laboratory technicians or equivalent	Appropriately trained and experienced personnel familiar with use of computers and automation in general
Servicing	QIAGEN Field Service Specialists only	

3. General Description

3 General Description

The QIAxcel Advanced system performs fully automated separation of DNA fragments, as well as RNA and proteins according to their molecular weight and can process up to 96 samples without user intervention. The QIAxcel Advanced system consists of the QIAxcel Advanced instrument, a QIAxcel Kit (containing a QIAxcel gel cartridge and reagents), a computer, and QIAxcel ScreenGel® software, which have been optimized to work together across a wide variety of applications and provide unmatched resolution, speed, and throughput for DNA, RNA, and protein analysis.

The QIAxcel ScreenGel software supplied with the QIAxcel Advanced provides both electropherograms and gel images of the nucleic acid and protein separation and can be used to perform the following types of analysis:

- Determination of the size and concentration of DNA fragments
- Determination of the ratio, concentration, and quality of total RNA, and the quality of cRNA/ cDNA and fragmented RNA/DNA
- Determination of protein size and concentration

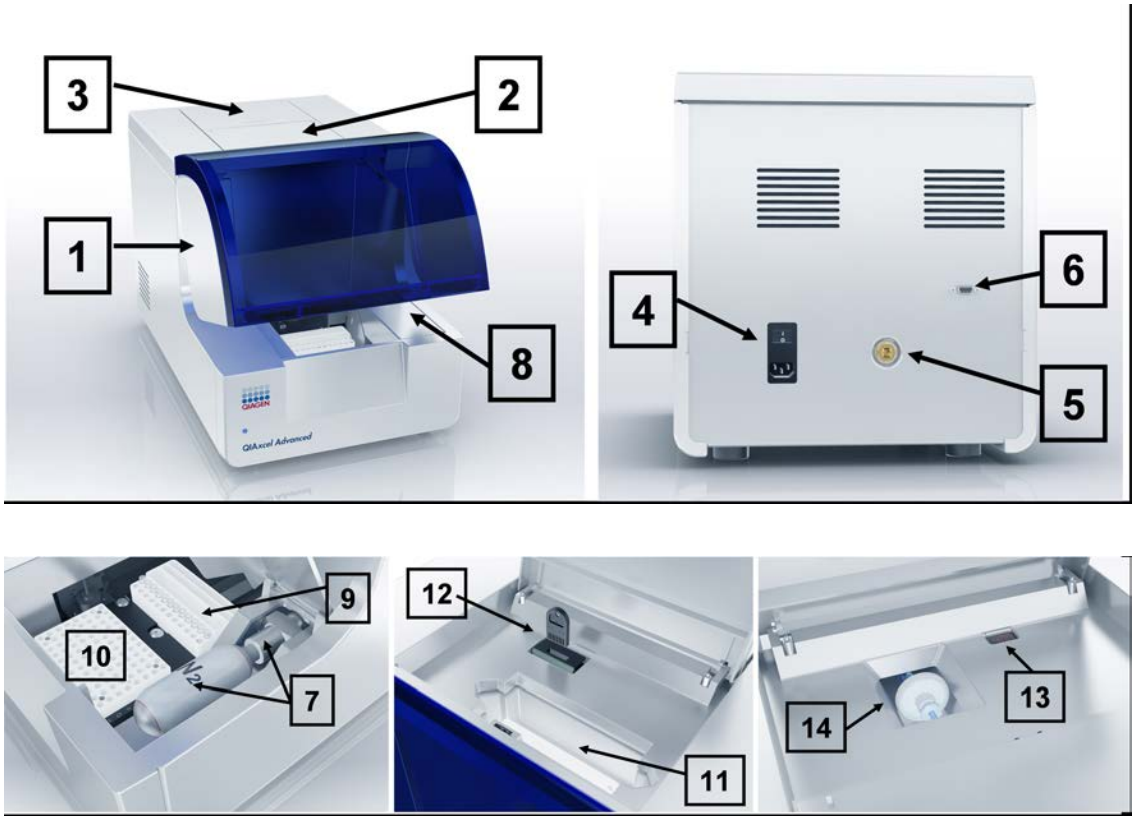
Note: We do not recommend determining nucleic acid concentration with the QIAxcel DNA Fast Analysis Kit.

3.1 QIAxcel Advanced principle

The QIAxcel Advanced uses capillary electrophoresis to enable high resolution and sensitive separation of DNA, RNA, and protein samples. This 12-channel capillary electrophoresis instrument uses disposable, multiple-use cartridges for cost-effective analysis of up to 96 samples in as little as 25 minutes.

1. The QIAxcel Advanced is set up with a gel cartridge, running buffer, and wash buffer, and calibrated using intensity markers.
2. The samples for analysis (in a 96-well plate or 12-tube strips) are placed onto the sample plate holder.
3. Required data collection settings are selected and the samples pass through the capillaries of the QIAxcel gel cartridge.
4. Data is analyzed using the QIAxcel ScreenGel software.

3.2 External features of the QIAxcel Advanced



External features of the QIAxcel Advanced.

1	Sample door	8	N_2 door
2	Cartridge door	9	Transport lock and buffer tray location
3	Service door	10	Sample plate holder
4	Power connection for AC connection	11	Cartridge bay
5	Tube fitting for external N_2 supply	12	Slot for smart key
6	RS232 connection	13	Digital pressure display
7	N_2 regulator and cylinder	14	Purge filter

Note: If using an external N_2 source, the output pressure must not exceed 75 psi. The QIAxcel Advanced is equipped with an internal regulator that will regulate the pressure provided by the external N_2 source to approximately 40 psi (37–45 psi), which is the instrument's operating pressure.

3.3 Gel cartridges

The QIAxcel Advanced can be operated using any of the QIAxcel Kits listed in the table below. Each kit contains a gel cartridge that has been specifically developed for particular applications. Each gel cartridge consists of a gel matrix with a proprietary linear polymer with, and in the case of DNA and RNA gel cartridges, ethidium bromide intercalating dye.

Kit	Application
QIAxcel DNA High Resolution Kit (1200)	Analysis of DNA 15 bp – 10 kb in size. 96 samples can be analyzed in <1.5 hours
QIAxcel DNA Screening Kit (2400)	Fast analysis of DNA 15 bp – 5 kb in size. 96 samples can be analyzed in just 40 minutes
QIAxcel DNA Fast Analysis Kit (3000)	Routine evaluation of DNA fragments in qualitative single or multiplex PCR applications. 96 samples can be analyzed in approximately 25 minutes.
QIAxcel RNA QC Kit v2.0 (1200)	Analysis of RNA quality and quantity. 96 samples can be analyzed in <1.5 hours
QIAxcel Protein Kit (1200)	Analysis of protein size, quantity, and purity. 96 samples can be analyzed in 2 hours.

Each QIAxcel Kit contains the following additional reagents that are required for use of the QIAxcel Advanced:

- QX Intensity Calibration Marker — calibrates the signal intensity for each new gel cartridge
- QX DNA, RNA, or Protein Separation Buffer (QIAxcel DNA, RNA, or Protein Kits) — enables separation of DNA, RNA, or proteins
- QX FA DNA Separation Buffer (QIAxcel DNA Fast Analysis Kit) — enables separation of DNA molecules (only for use with the QIAxcel DNA Fast Analysis Cartridge)
- QX Wash Buffer — for washing the capillary tips to prevent cross-contamination
- QX DNA or RNA Dilution Buffer — for optimization of sample concentration
- QX Mineral oil — for covering solutions and/or samples to prevent evaporation
- QX Alignment Marker — used in every run to equalize the migration time variation across all channels (included in the QIAxcel RNA QC Kit v2.0, QIAxcel Fast Analysis Kit, and QIAxcel Protein Kit only; for all other kits, see ordering information, Appendix C)

Note: QIAxcel DNA Size Marker is required for use with QIAxcel DNA Kits only. This enables creation of a reference marker table allowing DNA size and concentration to be determined (not included in kit; see ordering information, Appendix C). QIAxcel RNA Size Marker is provided with the QIAxcel RNA QC Kit v2.0. QX Pro Marker is provided with the QIAxcel Protein Kit.
In addition to the components listed above, the QIAxcel Protein Kit also contains QX Reduction Agent, QX Labeling Buffer, and QX Labeling Dye for sample preparation before electrophoresis.

3.4 Computer and software

The QIAxcel Advanced is shipped with QIAxcel ScreenGel software.

A computer with the correct specifications for operation of the QIAxcel Advanced instrument and QIAxcel ScreenGel software is supplied as part of the QIAxcel Advanced system. However, if a different computer is used to operate the QIAxcel Advanced instrument or run the QIAxcel ScreenGel software, then the following requirements are necessary:

- Intel® Celeron® 540 CPU at 1.86 GHz or higher
- 80 GB free hard drive capacity, NTFS formatted
- 512 MB RAM
- 1024 x 768 screen resolution or higher
- 9-PIN Serial Port or
  I/O card (not provided, contact QIAGEN Technical Services for more information).
- Microsoft® Windows® XP Professional with Service Pack 3 or
  Microsoft Windows 7 Professional
- Adobe® Reader® software 8.2 or higher (for reading PDF reports)

This page intentionally left blank

4. Installation Procedures

4 Installation Procedures

This section provides instructions on unpacking and installing the QIAxcel Advanced.

4.1 Requirements

This section of the QIAxcel Advanced User Manual specifies the requirements for operating the QIAxcel Advanced.

4.1.1 Site

The QIAxcel Advanced must be located out of direct sunlight, away from heat sources, and away from sources of vibration and electrical interference. Refer to Appendix A for the operating conditions (temperature and humidity). The site of installation should be free of excessive drafts, excessive moisture, excessive dust, and not subject to large temperature fluctuations.

Use a level workbench that is large enough to accommodate the QIAxcel Advanced and computer. Refer to Appendix A for the weight and dimensions of the QIAxcel Advanced.

Ensure that the workbench is dry, clean, vibration-proof, and has additional space for accessories. Approximately 72 cm (28 in.) clearance above the workbench is recommended to allow cartridge loading.

The QIAxcel Advanced must be placed within approximately 1.5 m (4.92 ft.) of a properly grounded (earthed) AC power outlet. The power line to the instrument should be voltage regulated and surge protected.

Note: We recommend plugging the instrument directly into its own wall socket and not to share the socket with other lab equipment. To achieve proper capillary electrophoresis separation, do not place the QIAxcel Advanced on a vibrating surface or near vibrating objects.

WARNING	**Explosive atmosphere** **[W5]** The QIAxcel Advanced is not designed for use in an explosive atmosphere.

WARNING	**Risk of overheating** **[W10]** To ensure proper ventilation, maintain a minimum clearance of 10 cm (3.94 in.) at the sides and rear of the QIAxcel Advanced. Slits and openings that ensure the ventilation of the QIAxcel Advanced must not be covered.

4.1.2 Power requirements

The QIAxcel Advanced operates at:

- 100–240 V AC, 50–60 Hz, 360 VA

Ensure that the voltage rating of the QIAxcel Advanced is compatible with the AC voltage available at the installation site. Main supply voltage fluctuations are not to exceed 10% of nominal supply voltages.

4.1.3 Grounding requirements

To protect operating personnel, the instrument is equipped with a 3-conductor AC power cord. To preserve this protection feature, do not operate the instrument from an AC power outlet that has no ground (earth) connection.

For replacement of the 3-conductor AC power cord, contact QIAGEN Technical Services for an authorized spare part.

4.2 Unpacking the QIAxcel Advanced

Before unpacking the QIAxcel Advanced, move the package to the site of installation and check that the arrows on the package point upward. In addition, check whether the package is damaged. In case of damage, contact the transporter of the package.

When lifting up the QIAxcel Advanced, slide your fingers under both sides of the instrument and keep your back straight.

WARNING	**Risk of personal injury and material damage** **[W2]** The QIAxcel Advanced is too heavy to be lifted by one person. To avoid personal injury or damage to the instrument, do not lift the instrument alone.

After unpacking the QIAxcel Advanced, check that the following documents are supplied:

- Packing list
- Warranty registration form
- *QIAxcel Advanced User Manual*
- Quick-start guide

Read the packing list to check that you have received all items. If anything is missing, contact QIAGEN Technical Services.

Check that the QIAxcel Advanced is not damaged and that there are no loose parts. If anything is damaged, contact QIAGEN Technical Services. Make sure that the QIAxcel Advanced has equilibrated to ambient temperature before operating it.

Retain the package in case you need to transport or ship the QIAxcel Advanced in the future. Instructions for packing the QIAxcel Advanced are given in section Packing the QIAxcel Advanced. Using the original package minimizes damage during transportation of the QIAxcel Advanced.

Carefully place the QIAxcel Advanced onto the workbench where it will be used. For site requirements please refer to section Requirements.

4.3 Installing the QIAxcel Advanced

Before operating the QIAxcel Advanced:

- The transport lock must be removed
- The power cord must be installed
- The N_2 cylinder or an external N_2 supply must be installed

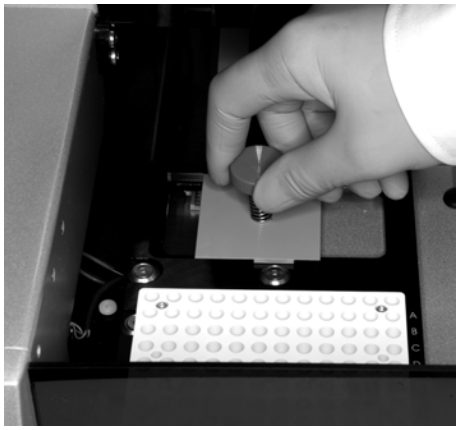
4.3.1 Releasing the transport lock

The QIAxcel Advanced is delivered with a transport lock that secures the tray/transport mechanism during shipment. This transport lock must be removed before the QIAxcel Advanced can be operated.

Note: Please reinstall the transport lock whenever shipping the instrument.

Remove the transport lock as follows:

1. Open the sample door.
2. Release the transport lock securing the buffer tray/sample plate holder.
3. Keep the transport lock in case you need to transport the QIAxcel Advanced in the future.



Removing the transport lock.

4.3.2 Instrument setup

Set up the QIAxcel Advanced as follows:

1. Set up the computer and monitor as described in the computer installation instructions provided with the computer.
2. Connect the RS232 serial cable from the instrument to the computer.

4.3.3 Installation of AC power cord

Connect the QIAxcel Advanced to the power outlet as follows:

1. Ensure that the power switch of the QIAxcel Advanced is set to the off position.
2. Check that the voltage rating on the label at the back of the QIAxcel Advanced matches the voltage available at the installation site.
3. Plug the power cord into the power cord socket at the rear of the instrument.
4. Plug the power cord into a grounded power outlet.

4.3.4 Installation of the N2 cylinder

Important: Use only N_2 cylinders provided by QIAGEN (cat. no. 929705).

1. Ensure that the power switch of the QIAxcel Advanced is set to the off position.
2. Open the N_2 door and gently pull up on the N_2 cylinder port. Do not pull past the detent hole.
3. Screw the N_2 cylinder into the port clockwise.
4. Turn until the needle inside the port punctures the N_2 cylinder. Do not overtighten; the cylinder should only be finger tight.
5. Gently push down on the N_2 cylinder until it is in its stowed (down) position.
6. Close the N_2 door.

Alternatively, use an external N_2 supply and attach to the rear of the instrument.

4.3.5 Installation of the QIAxcel ScreenGel software

For computer system requirements, refer to section Computer and software.

If you need to install the QIAxcel ScreenGel software, follow the steps below.

1. Uninstall a prior installation of the QIAxcel ScreenGel software through the Windows Control Panel.
2. Place the CD in the computer's CD-ROM drive.
3. The setup wizard will automatically start installation of the QIAxcel ScreenGel software and will guide you through the setup process.

   Important: If the setup wizard does not start automatically, double-click on "My Computer" and double-click on the CD-ROM drive. Launch the **setup.exe** program. This will start the QIAxcel ScreenGel software installation.
4. Accept the license agreement.
5. Select the program installation path. The default path is C:\Program Files\QIAGEN\QIAxcel\ScreenGel.
6. Select the data path for acquired data and all other application data. The default path is:
   - C:\Documents and Settings\All Users\Application Data\QIAGEN\QIAxcel\ScreenGel for Microsoft Windows XP Professional
   - C:\ProgramData\QIAGEN\QIAxcel\ScreenGel for Microsoft Windows 7 Professional

   Note: It is not possible to choose C:\Program Files\QIAGEN\QIAxcel\ScreenGel also as the data path. It is also not possible to choose the system root path (e.g., C:\Windows) as the data path.

   Note: Reference markers that were created with a previous version of the QIAxcel ScreenGel software will be removed during installation. Recreate the reference marker from the appropriate size marker runs.

   Note: All paths in this manual refer to the data path as %DATA_DIR%.

   Note: The %DATA_DIR% directory and its subdirectories can be opened in the windows explorer directly from QIAxcel ScreenGel software, through the menu item "File/Open Data Directory".
7. After the installation, the QIAxcel ScreenGel software can be started either from the Windows start menu under "QIAGEN/QIAxcel" or from the desktop icon.

Note: QIAxcel ScreenGel uses several software packages provided by Microsoft. If they are not installed on the system, these software packages are automatically installed at the beginning of the QIAxcel ScreenGel software setup. When the respective dialog box is shown, click the "Install" button to install these required software packages.
Depending on the installed software packages, a reboot of the system may be required before proceeding with the setup. After the reboot, the installation procedure is resumed automatically.

4.3.6 Getting started with the QIAxcel ScreenGel software

Before using the software, read the Concepts of QIAxcel ScreenGel. Afterwards, configure the software. This can only be carried out by a user with the "Administrator" role.

1. Launch the QIAxcel ScreenGel software from the Windows start menu in the "QIAGEN"/"QIAxcel" folder or from the desktop icon.
2. Log in as "Administrator" and click "OK" (for this first login, no password is required).
3. Provide a valid password for the "Administrator" account. Leave the field for the old password empty, then provide a new valid password and enter it again.

   Note: The password must contain one upper-case character, one lower-case character, and one digit. The minimum size of the password is eight characters.
4. The "Configuration" environment is displayed by default. Select the "User Manager" tab.
5. Create user accounts for all relevant users. For more information, refer to User management and User roles.
6. Configure which COM port is to be used for connection to the QIAxcel Advanced system. The default adjustment is COM1. For more detailed information, refer to Settings.
7. Configure the global settings for the QIAxcel ScreenGel software. For further details, refer to Settings.

4.4 Packing the QIAxcel Advanced

WARNING/ CAUTION	**Risk of personal injury and material damage** [W2] The QIAxcel Advanced is too heavy to be lifted by one person. To avoid personal injury or damage to the instrument, do not lift the instrument alone.

If you need to transport the QIAxcel Advanced, pack the instrument as follows:

1. Switch on the QIAxcel Advanced.
2. Switch on the computer and launch the QIAxcel ScreenGel software.
3. Click in the "Status Information" panel to move the buffer tray to the front of the instrument.
4. Open the sample door and remove the buffer tray.
5. Remove the QIAxcel gel cartridge from the QIAxcel Advanced and store in the QX Cartridge Stand as described in section Unpacking a QIAxcel Kit.
6. Remove the N_2 bottle as described in section N_2 cylinder replacement.
7. Close the QIAxcel ScreenGel software and switch off the QIAxcel Advanced.

8. Disconnect the RS232 serial cable from the instrument to the computer and remove the AC power cord.
9. Reinstall the transport lock holding down the sample plate holder (see section Installing the QIAxcel Advanced).
10. Place the QIAxcel Advanced into the original packaging it was shipped in.

5. Operating Procedures

5 Operating Procedures

This section describes how to operate the QIAxcel Advanced.

Before proceeding, we recommend that you familiarize yourself with the features of the QIAxcel Advanced by referring to the section General Description.

The QIAxcel Advanced cartridge door, sample door, and service door must remain closed during operation of the instrument. Only open the doors when the instrument is not operating or when instructed to do so by the software.

Note: Opening the cartridge door or sample door during operation of the QIAxcel Advanced will cause the system to stop the action it is currently performing. Any sample run in progress cannot be recovered. However, due to the small volume of sample used, a new run can be performed.

WARNING	**Risk of personal injury and material damage** [W3] Do not attempt to move the QIAxcel Advanced during operation.

WARNING	**Moving parts** [W9] To avoid contact with moving parts during operation of the QIAxcel Advanced, the instrument must be operated with the cartridge door and sample door closed. If the door sensors are not functioning correctly, contact QIAGEN Technical Services.

5.1 Unpacking a QIAxcel Kit

1. Carefully read the handbook supplied with the QIAxcel Kit before starting.
2. Remove all buffer bottles from the kit. Refer to the handbook for a detailed description of the kit contents.
3. Add 10 ml QX Wash Buffer to both reservoirs of the QX Cartridge Stand (provided with the QIAxcel instrument) reservoir and cover it with 2 ml mineral oil.
4. Remove the QIAxcel gel cartridge from its packaging and carefully wipe off any soft gel debris from the capillary tips using a soft tissue.

   Note: The QIAxcel gel cartridge is provided together with a smart key, which is used for fully automatic cartridge detection. Do not remove the smart key from the cartridge.
5. Remove the purge cap seal from the back of the QIAxcel gel cartridge and place it in the QX Cartridge Stand.

   Note: A soft tissue should be used to wipe off any gel that may have leaked from the port.

   Note: Ensure that the capillary tips are submerged in QX Wash Buffer.
6. New cartridges should be allowed to stand at room temperature in the QX Cartridge Stand for at least 20 minutes prior to use. Protect the cartridge from light with the QX Cartridge Stand Cover when the cartridge is in the stand. Prior to use, the QIAxcel gel cartridge should be placed into the QX Cartridge Stand, or stored latched in the instrument in the "Park" position with buffer in the buffer tray, and allowed to stand for at least 20 minutes.

QIAxcel Gel Cartridge in the QX Cartridge Stand.

5.2 Setting up the QIAxcel Advanced

The steps required for correct setup of the QIAxcel Advanced instrument before each use are described in this section.

5.2.1 Preparing the buffer tray

Important points before starting

- If using pre-aliquoted alignment marker, the 12-tube strip containing QX Alignment Marker should be equilibrated to room temperature (15–25°C) and centrifuged briefly before use.
- When using QIAxcel DNA Kits, we recommend changing the alignment markers every 50 runs or 3 days, whichever comes first. Additional markers and buffers may need to be purchased (see ordering information in Appendix C).
- When using the QIAxcel RNA QC Kit v2.0, we recommend changing the alignment markers every 15–20 runs or 3 days, whichever comes first. Additional markers and buffers may need to be purchased (see ordering information in Appendix C).
- When using the QIAxcel Protein Kit, we recommend changing the alignment markers every 24 runs (or after three 96-well plate runs).
- When not in use, store the 12-tube strip containing QX Alignment Marker and the QX Pro Alignment Marker at –20°C.
- The volumes of QX Separation Buffer and QX Wash Buffer provided are sufficient for the maximum number of runs stated on the gel cartridge.

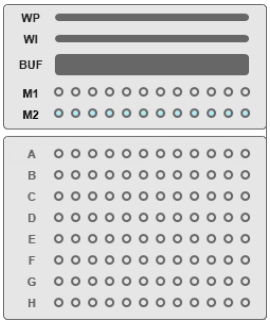
- The 12-tube strips should fit loosely in the "MARKER1" and "MARKER2" positions. Tightly fitting tube strips or tube strips that are too loose may cause injection problems and damage the cartridge capillaries.
- Allow all reagents to equilibrate to room temperature before use.

Procedure

1. Wash the buffer tray in warm water using a mild detergent and rinse thoroughly with deionized or reverse-osmosis water.
2. Fill the positions of the buffer tray as listed below:

Cartridge type	Buffer tray position		
	Wash Park (WP)	Wash Inject (WI)	Buffer (BUF)
DNA High Resolution	8 ml QX Wash Buffer	8 ml QX Wash Buffer	18 ml QX DNA Separation Buffer
DNA Screening	8 ml QX Wash Buffer	8 ml QX Wash Buffer	18 ml QX DNA Separation Buffer
DNA Fast Analysis	8 ml QX Wash Buffer	8 ml QX Wash Buffer	18 ml QX FA DNA Separation Buffer
RNA	8 ml QX Wash Buffer	8 ml QX Wash Buffer	18 ml QX RNA Separation Buffer
Protein	8 ml QX Wash Buffer	8 ml distilled water	18 ml QX Pro Separation Buffer

3. Add QX Mineral Oil to cover all 3 positions to prevent evaporation. Add 2 ml QX Mineral Oil to positions "WP" and "WI", and add 4 ml QX Mineral Oil to the position "BUF".
4. Load 15 µl QX Alignment Marker into each well of a QX 0.2 ml 12-Tube Strip or use a pre-aliquoted strip.
5. Add 1 drop of QX Mineral Oil to each well and insert the strip into the "M1" position of the buffer tray.
6. If the cartridge is not calibrated yet, load 15 µl QX Intensity Calibration Marker when using the QIAxcel DNA or RNA Kit, or 15 µl QX Pro Calibration Marker when using the QIAxcel Protein Kit, into each well of a QX Color 0.2 ml 12-Tube Strip. Add a drop of QX Mineral Oil, and insert the strip into the "M2" position of the buffer tray.



Buffer tray

5.2.2 Loading the buffer tray

If not already carried out:

1. Switch on the QIAxcel Advanced at the power switch.
2. Switch on the computer, launch the QIAxcel ScreenGel software from the Windows start menu under "QIAGEN/QIAxcel" or from the desktop icon.
3. In the QIAxcel ScreenGel software, select a mode (DNA, RNA, or protein) and log in (for detailed information refer to the User authentication section). The "Process" environment opens and displays the first screen of the process profile of the process wizard.

   Note: The icon indicates that the connection is being established and the icon shows that the QIAxcel Advanced is connected.

To load the buffer tray proceed as follows:

1. Close the cartridge door and the sample door.

   Note: The QIAxcel Advanced cartridge and sample doors must remain closed during operation of the instrument. Opening either door during operation will cause the system to stop any action it is currently performing.

2. Click in the "Status Information" panel at the left to move the buffer tray holder to the front of the instrument. Wait until the buffer tray holder has reached its stop position.
3. Open the sample door.
4. Carefully place the filled buffer tray into the buffer tray holder. Be careful not to spill any solutions in the instrument or cause any cross-contamination between buffers loaded on the buffer tray.

   Note: The 12-tube strips should be positioned towards the front of the instrument with the buffers towards the back.

5. Close the sample door and click in the "Status Information" panel to move the buffer tray holder to the "Wash Park" position.

   Note: Leave the sample door open if you want to load your samples immediately afterward.

   Note: If you close the sample door, the buffer tray automatically moves to the "Wash park" position after a period of 5 minutes.

5.2.3 Installing a QIAxcel gel cartridge and smart key

Note: Read section Unpacking a QIAxcel Kit prior to performing this procedure.

1. Remove the QIAxcel gel cartridge from the QX Cartridge Stand.
2. Open the cartridge door and insert the QIAxcel gel cartridge into the QIAxcel Advanced. The cartridge description label should be facing toward the front and the purge hole should be toward the rear of the instrument.

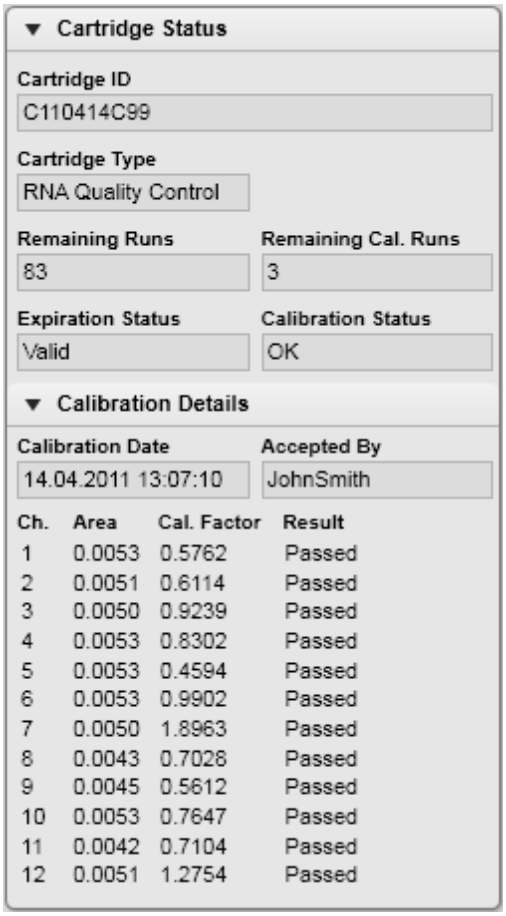
   Note: Ensure the purge cap seal has been removed as described in Unpacking a QIAxcel Kit.

3. Insert the smart key into the smart key socket near the cartridge. The smart key can be inserted in either direction.

   Note: The system will not recognize the cartridge and will not operate if the smart key is not inserted.

Note: If the settings option "Latch cartridge automatically" is selected, the cartridge will be automatically latched after the smart key is detected. Therefore, it is important to insert the smart key as soon as the cartridge has been inserted and the cartridge door has been closed. Refer to section Settings for information about settings.

4. Close the cartridge door.
   The cartridge ID and cartridge type will be displayed automatically in "Cartridge Status" in the "Status Information" panel.



Cartridge status area.

5.2.4 Removing a QIAxcel gel cartridge

To remove a QIAxcel gel cartridge from the QIAxcel Advanced proceed as follows:

1. Prepare the QX Cartridge Stand as described in section Unpacking a QIAxcel Kit.
2. Open the cartridge door.
3. Remove the smart key.

   Note: If the settings option "Latch cartridge automatically" is selected, the cartridge will be unlatched automatically after the smart key is removed. Therefore, it is important to remove the smart key first before trying to remove the cartridge. Refer to section Settings for information about settings.

   Note: If the QIAxcel Advanced is switched on and "Latch cartridge automatically" is unchecked, ensure the QIAxcel gel cartridge is unlatched. If latched, unlatch it. See section "Status Information" panel for information about how to do this.
4. Remove the QIAxcel gel cartridge.
5. Install the purge cap seal to close the purge port.
6. Place the QIAxcel gel cartridge in the QX Cartridge Stand.

   Note: Ensure that the capillary tips are submerged in QX Wash Buffer.

5.2.5 Storing a QIAxcel gel cartridge

Storage of QIAxcel DNA gel cartridges after delivery

All components of the **QIAxcel DNA High Resolution Kit**, and the **QIAxcel DNA Screening Kit**, except for the gel cartridge and the QX Intensity Calibration Marker, can be stored dry at room temperature (15–25°C) and are stable until the expiration date under these conditions.

The QIAxcel gel cartridge and the QX Intensity Calibration Marker should be stored at 2–8°C upon arrival and are stable until the expiration date under these conditions.

All components of the **QIAxcel DNA Fast Analysis Kit** can be stored dry at room temperature, except for the QIAxcel gel cartridge, QX Intensity Calibration Marker, QX DNA Size Marker 50 bp – 1.5 kb, and QX Alignment Marker 15 bp/3 kb. The QIAxcel gel cartridge and the markers should be stored at 2–8°C upon arrival. Components are stable until the expiration date under the indicated conditions.

Storage of the QIAxcel RNA gel cartridge after delivery

Note: QX RNA Denaturation Buffer and QX RNA Size Marker 200–6000 nt are delivered separately.

QX RNA Size Marker 200–6000 nt should be stored at –20° to –80°C, and is stable until the expiration date under these conditions.

QX RNA Denaturation Buffer should be stored at 2–8°C and is stable until the expiration date under these conditions.

All other components of the QIAxcel RNA QC Kit v2.0, except for the QIAxcel gel cartridge, can be stored dry at room temperature (15–25°C) and are stable until the expiration date under these conditions.

The QIAxcel gel cartridge should be stored at at 2–8°C and is stable until the expiration date under these conditions.

Storage of the QIAxcel Protein gel cartridge after delivery

The QIAxcel Protein Kit (1200) comprises the QIAxcel Protein Cartridge Kit and the QIAxcel Protein Reagent Kit.

Note: The QIAxcel Protein Reagent Kit includes marker, reduction agent, and dye, and is delivered separately. These components should be stored at 2–8°C and are stable until the expiration date under these conditions.

All other components delivered with the QIAxcel Protein Cartridge Kit should be stored dry at room temperature (15–25°C) and are stable until the expiration date under these conditions.

Occasional use

Store QIAxcel DNA and RNA gel cartridges at 2–8°C until the first use and the QX Protein gel cartridge at room temperature (15–25°C) until the first use. If the QIAxcel gel cartridge is not being used on a daily basis, close the purge port with the purge port seal, return the gel cartridge to the blister package, inserting the capillary tips into the soft gel. Store the QIAxcel DNA or RNA gel cartridge at 2–8°C and the QIAxcel Protein gel cartridge at room temperature in an upright position (see orientation label on blister package).

Note: Storing the QIAxcel DNA or RNA gel cartridge below 2°C and the QIAxcel Protein gel cartridge below 15°C can severely damage the cartridge.

Prior to use, the QIAxcel gel cartridge should be placed into the QX Cartridge Stand and protected with the cover whenever exposed to light, and allowed to stand for at least 20 minutes at room temperature.

Daily use

If the QIAxcel gel cartridge is being used on a daily basis, store the cartridge latched in the QIAxcel Advanced in the “Park Position”.

Note: The QIAxcel Advanced must be left on if the cartridge is stored in the “Park Position” and the cartridge must be latched. Do not switch the QIAxcel Advanced off.

If more than one QIAxcel gel cartridge is being used on a daily basis, store the second cartridge in the QX Cartridge Stand in the dark or protected with the cover. Make sure that the cartridge stand reservoir is filled with wash buffer and covered with mineral oil (refer to Unpacking a QIAxcel Kit). Alternatively, close the purge port with the purge port seal, return the QIAxcel gel cartridge to the blister package, inserting the capillary tips into the soft gel, and store the QIAxcel gel cartridge at room temperature in an upright position (see orientation label on blister package).

The QIAxcel gel cartridge can be stored in this manner until expiration date as indicated on the kit label.

5.3 Operating the QIAxcel Advanced

Samples are processed using the "Process" environment of the QIAxcel ScreenGel software.

Depending on the role of the user logged in, the environments behave differently. Users with the "Routine User" role are guided step by step to start a process. Users with the "Advanced User" role will not be guided step by step, they can freely define analysis and process profile parameters when starting a run.

This section describes the operating procedure of the QIAxcel Advanced for the routine user. Advanced features of the QIAxcel ScreenGel software, which are not available to the routine user, are described in the Process section.

5.3.1 Things to do before starting

- Carefully read the handbook supplied with the QIAxcel Kit.
- Prepare the reagents and QX Alignment Marker to be used. For instructions about how to do this, see section Setting up the QIAxcel Advanced, or refer to the QIAxcel Kit handbook.

  Note: Refer to steps 1, 2, 3, 4, 7, and 8 in Running procedure for information about the alignment marker or size marker. These steps can be skipped later. The alignment marker required is displayed in the software and can now be prepared.
- Prepare your samples. Refer to the handbook supplied with the QIAxcel Kit for instructions about how to do this. For optimal results, the sample solution should be pH 6–9 and should not have an ionic content greater than that of a typical PCR buffer.

  Note: If you need to run a size marker side by side with the samples, prepare it in the required position on the sample plate. Refer to the handbook supplied with the QIAxcel Kit for instructions about how to do this.

CAUTION	**Damage to the cartridge** [C4] If less than 12 samples are processed, fill the empty sample wells with QX DNA Dilution Buffer, QX RNA Dilution buffer, or QX Pro Labeling Buffer, respectively. Failure to do so may cause damage to those particular capillary channels.

5.3.2 Starting a run

Routine users can run predefined "Process Profiles" using the process wizard of the QIAxcel ScreenGel software only (for advanced process options refer to section Running a process with advanced options). Follow these steps to perform runs as a routine user:

1. Switch on the QIAxcel Advanced at the power switch.
2. Switch on the computer, launch the QIAxcel ScreenGel software from the Windows start menu under "QIAGEN/QIAxcel" or from the desktop icon.
3. In the QIAxcel ScreenGel software, select a mode (DNA, RNA, or protein) and log in (for detailed information refer to the User authentication section). The "Process" environment opens and displays the first screen of the process profile of the process wizard.

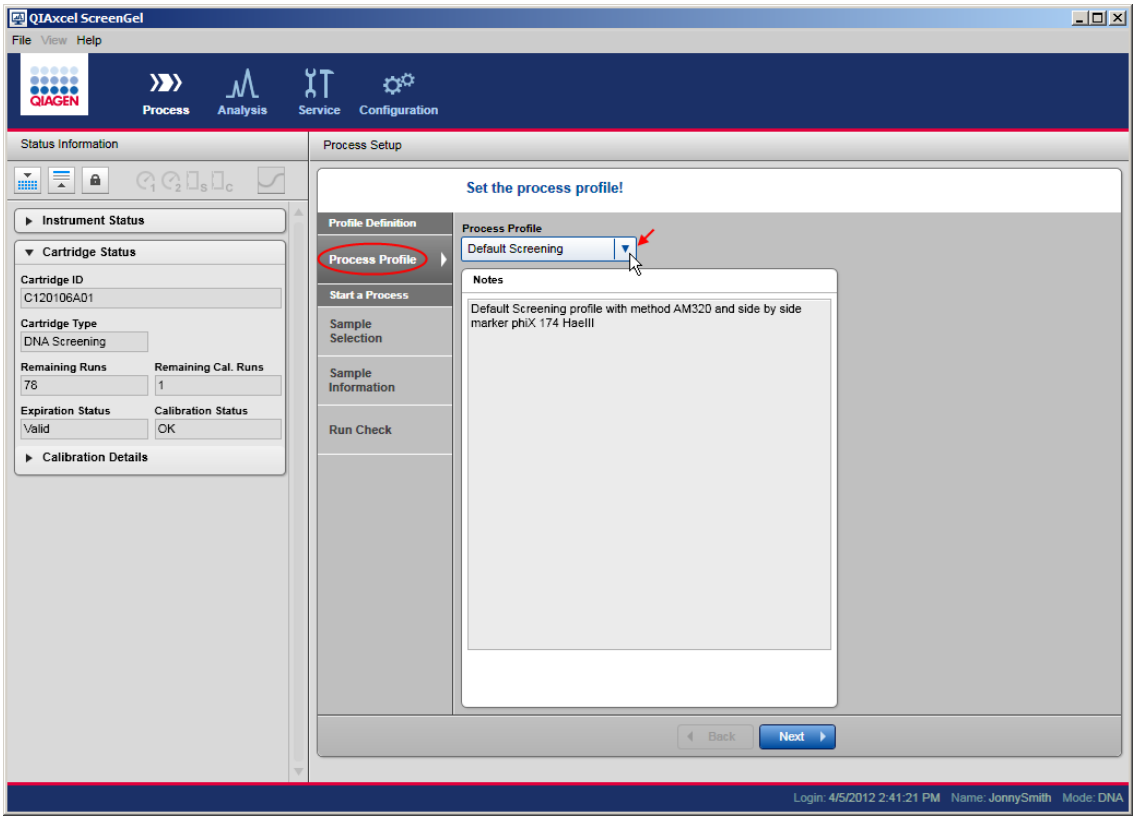
   Note: The icon indicates that the connection is being established and the icon shows that the QIAxcel Advanced is connected.
4. Install the QIAxcel gel cartridge to be used as described in Installing a QIAxcel Gel Cartridge and smart key.

   Note: You can inspect the cartridge status in the "Status Information" panel to the left of the "Process" environment. Refer to the "Status Information" panel section for detailed information.
5. Place the buffer tray containing the QX Alignment Marker onto the buffer tray holder as described in Loading the buffer tray.
6. Place the sample strips (in position A) or a 96-well plate onto the sample plate holder.

7. Close the sample door.

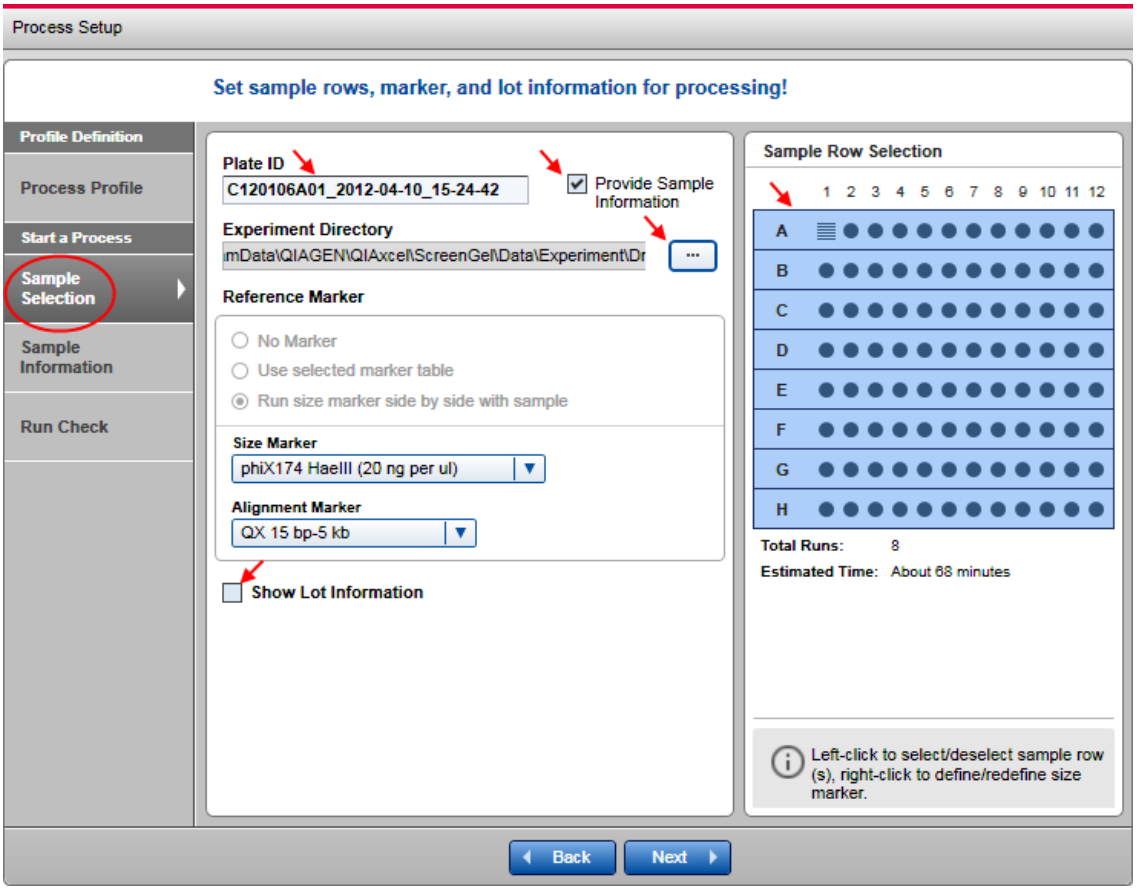
   Note: If the instrument doors are closed, the buffer tray automatically moves to the "Wash park" position after a period of 5 minutes.

8. In QIAxcel ScreenGel, select a predefined process profile in the "Process Profile" screen.



"Process Profile" screen.

9. Click the "Next" button to proceed to the next screen, "Sample Selection".



"Sample Selection" screen.

10. You can optionally change the directory where the experiment will be saved. This can be a local or a network directory.

    Note: The directory can only be changed if the process profile used allows it (see Selecting general process options).

11. Optionally, change the plate ID.

    Note: The plate ID will be used to name all the results from this process, for the experiment storing the sample data, as well as for generated report/export files. Therefore, a unique plate ID is required. See Run parameters and result structure for further information.

    Note: For the plate ID, the software allows alpha numeric characters only (this means that brackets, special letters such as ä or μ, and special characters such as /&!%$§ ' ´ ´ @*+~#=<>|;, etc cannot be used.) The software removes blanks at the start and at the end automatically.

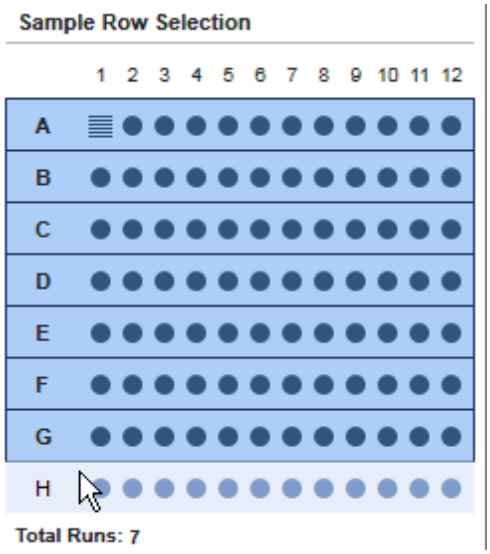
    Note: After the process, the plate ID cannot be modified.

    Note: If the settings option "Generate plate ID" is selected, the system automatically generates a plate ID following the rules specified in the settings. Refer to section Settings for more information. However, the plate ID may be modified.

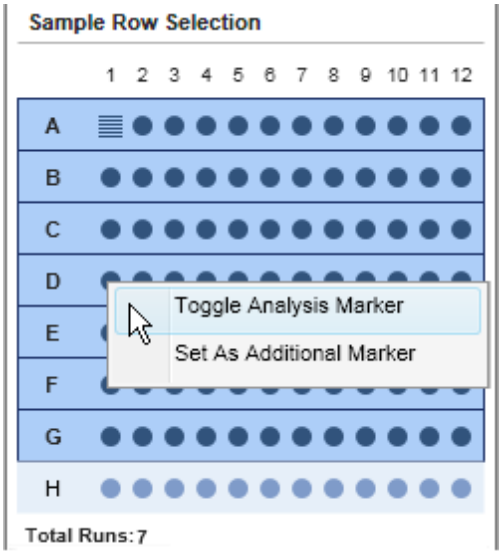
12. You can optionally change selection of sample rows to be processed. Use this option if you want to process less rows than specified in the process profile. Left-click the row to deselect/select.

Note: Changing sample rows is only possible if the process profile used allows it (see Selecting run parameters).

Note: It is not possible to deselect a row containing the size marker. If you want to do so, proceed to the next step first and then deselect the row.



Sample row H was deselected.



Changing the size marker position to D1.

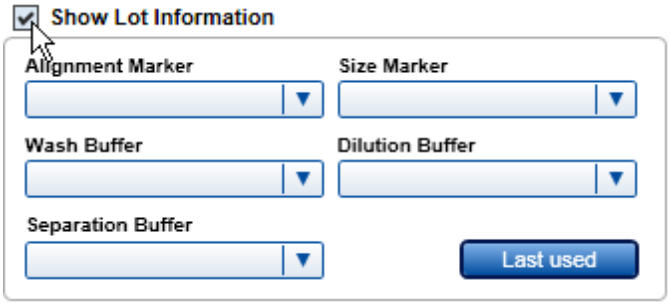
13. You can optionally change the position of the size marker on the plate, by right-clicking the new marker position. Select the option "Toggle Analysis Marker" from the context menu that appears. This size marker will be used for automatic analysis during process, if analysis is included in the process profile.

    Note: The size marker position can only be changed if the process profile used allows it (see Selecting run parameters).

    Optional: If you have an additional size marker in the sample plate, right-click the position and select the "Set as Additional Marker" option from the context menu. A rotated ladder symbol appears. Right-click again and select the "Size Marker Name" from the context menu. This information can be used for manual analysis, but will not be used for automatic analysis during the process.

14. If the "No marker" option is selected, select the prepared alignment marker from the "Alignment Marker" drop-down box. If you leave the "Alignment marker" drop-down box empty, you have to acknowledge a warning later in the "Run check" screen.

15. **Optional**: Provide lot information of buffers and markers by checking the "Show Lot Information" box and editing the lot information in the fields displayed.

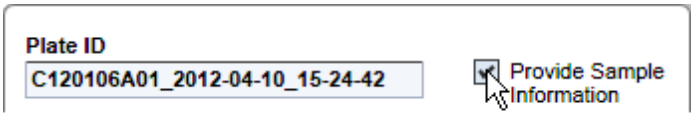


Visible lot information fields.

Note: This is available only if either the settings option "Enable input fields for Buffer lot IDs" or "... Marker lot IDs" is selected (see Settings).

Note: The last used lot information values can be selected from drop-down lists. Restore the last used combination of the lot information by clicking on the button "Last used".

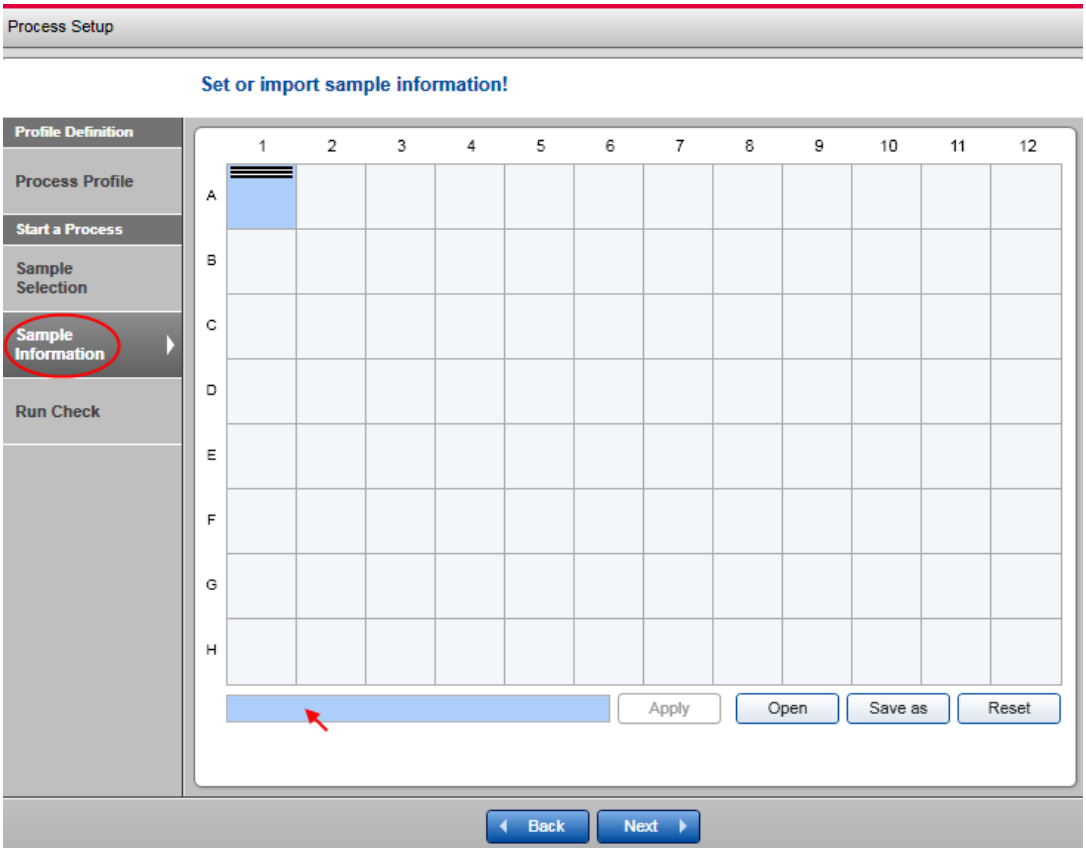
16. **Optional**: Check the "Provide Sample Information" box if you want to provide sample information. If not, proceed to step 19.



"Provide Sample Information" box checked.

Note: The "Sample Information" screen is enabled only if the check box is checked.

17. Click the "Next" button to proceed to the next screen, "Sample Information".



"Sample Information" screen.

18. **Optional**: Provide sample information, entered manually or imported from file.

    To provide sample information **manually**, enter the sample information starting at position A1 (preselected). The entered text is shown in the edit field below the table. Confirm the information for each position by pressing the "Enter" key; the next position will be selected automatically for the next input. To provide sample information for a selected position only, click the position, enter the sample information in the edit field, and confirm with the "Enter" key or click the "Apply" button.

    To save the provided sample information in a file for later reuse, click the "Save as" button. A dialog box will appear listing all available import files, which are stored in the "Sample Information" directory as configured in the settings. Navigate to the directory where the sample information will be stored, enter a file name, and click "OK".

    To import sample information **from a file**, click the "Open..." button. A dialog box appears and lists all available import files, which are stored in the "Sample Information" directory as configured in the settings. Navigate to the directory where the sample information was stored, select the import file, and click "OK". The imported data overwrites all sample information provided before.

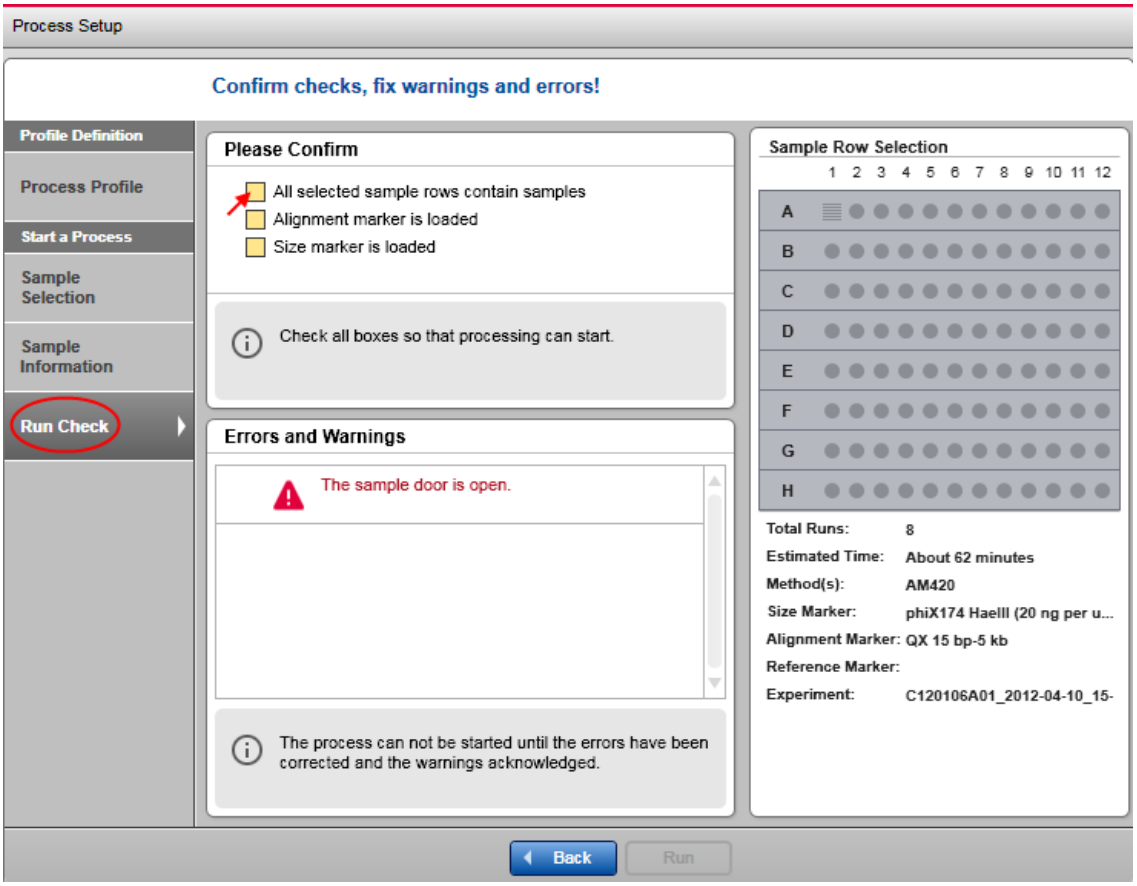
    For further information about editing sample information, refer to section Provide Sample Information.

    Note: The size marker positions are marked by a "ladder" symbol.

    Note: Click the "Reset" button to clear sample information; use the "Tab" key and "Shift"+"Tab" to navigate through the positions.

Note: Refer to section Settings for information about configuration details.

19. Click the "Next" button to proceed to the next screen, "Run Check".



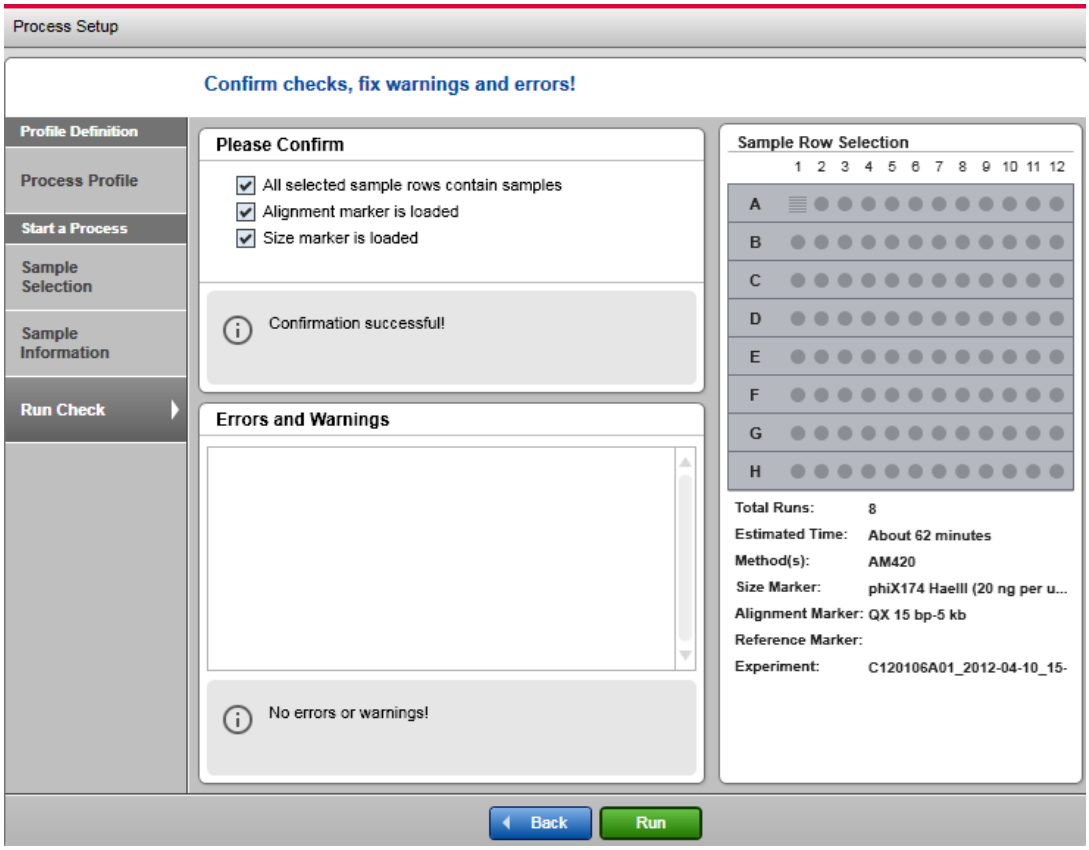
"Run Check" screen with "Sample door is open" error.

20. Confirm all check boxes. Resolve the problems indicated by warnings and errors. Use the "Back" and "Next" buttons to navigate.

    Note: The process can be started only when all run checks are confirmed and no errors/ warnings are shown.

    Note: A handover to an Advanced User may be required.

    Note: If the "Run" button is still deactivated, check the "Status Information" panel for cartridge and instrument status or refer to the Troubleshooting section.



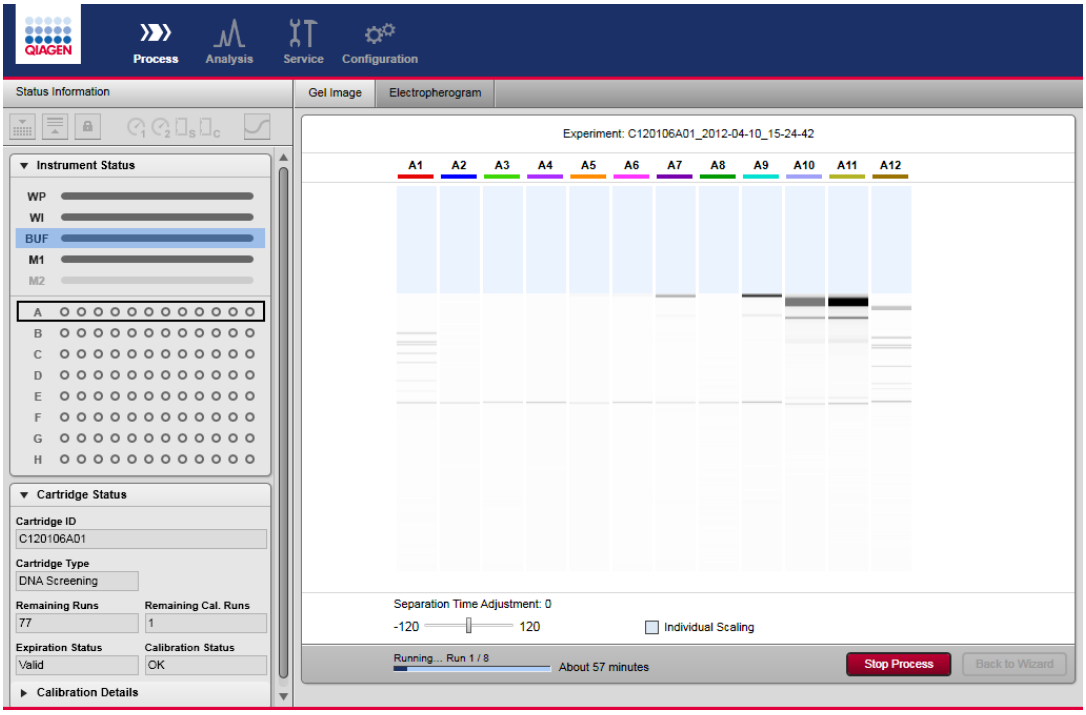
"Run Check" screen with all confirmation boxes checked and all problems resolved.

21. Start the process by clicking the "Run" button.

    The process wizard will be closed and a preview will be shown for each row currently processed. The actions performed by the instrument are shown in the "Instrument Status" panel on the left. A progress bar below the preview shows the progress of the whole process and the estimated remaining process time.

    Depending on the report settings the generated report may be displayed.

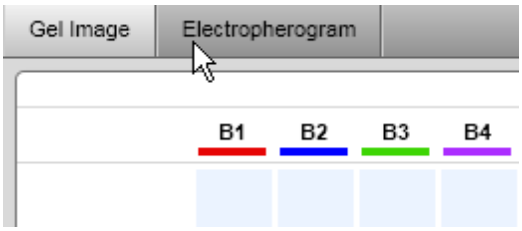
    Note: Opening the cartridge door or sample door during operation of the QIAxcel will cause the system to stop the action it is currently performing. The process is stopped and cannot be recovered. No sample data are stored for the row currently processed. Sample data are stored for completed rows only. No analysis, peak calling or report/export is performed. Thus, the stored sample data contain raw data only.



Process currently running row A.

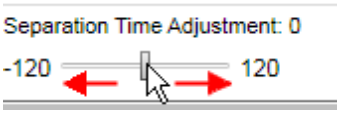
Actions during process run:

- You can switch between the gel and electropherogram preview by clicking the respective tab.



Switching from Gel Image to Electropherogram.

- Optionally adjust the separation time. To do so, move the "Adjust Separation Time" slider below the preview. Moving it to the extreme left position will shorten the separation time by 120 seconds, moving it to the extreme right position will extend the separation time by 120 seconds. Moving the slider takes effect for an actual ongoing separation as well as for all following separations during the process.



Adjust separation time.

Note: The slider can be moved either by using the mouse or by pressing the "Cursor left" or "Cursor right" key on the keyboard.

Note: When starting the next process by clicking the "Run" button, the slider is automatically reset to the middle position and the separation time will be applied as defined in the method.

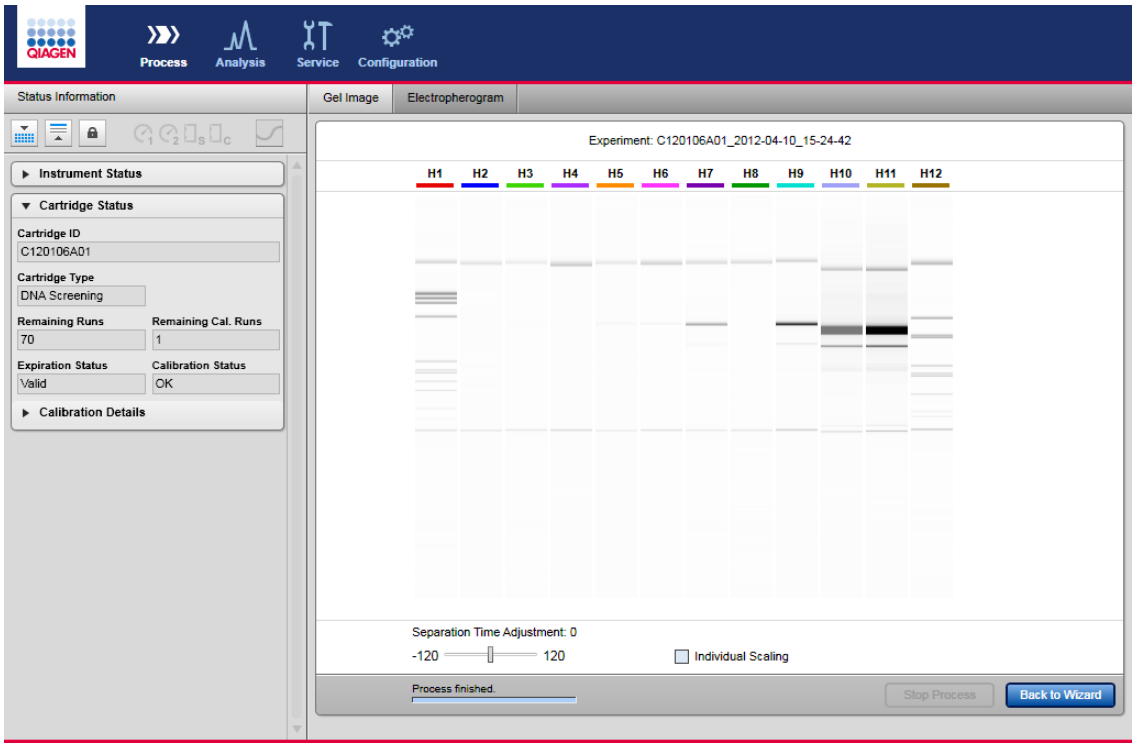
- Optionally switch the check box "Individual Scaling" on/off to adapted colors to the overall maximum signal height of all samples. See Gel view for more information about individual scaling. The check box "Individual Scaling" is off initially.

- The process can be stopped by clicking the "STOP" button below the preview.

  Note: If the instrument motors are currently moving, the process will stop after this movement.

  Note: No sample data are stored for the row processed. Sample data are stored for completed rows only. No analysis, peak calling, or report/export is performed. Thus the stored sample data contain raw data only.

Actions after the process has finished:



Process has finished.

- The next process can be started by returning to the process wizard, clicking the "Back to Wizard" button below the preview.
- To inspect the sample data switch to the analysis environment. For information how to do that refer to sections Environments, Handling samples and experiments and Viewing sample data respectively. Return to the process environment and click the "Back to Wizard" button to start the next process.

This page intentionally left blank

6. QIAxcel ScreenGel Software

6 QIAxcel ScreenGel Software

The user-friendly QIAxcel ScreenGel software has been specifically developed for use with the QIAxcel Advanced system. The software offers interactive tools that simplify data analysis, allow fast data interpretation, and provide flexibility in viewing data and results in both electropherogram and gel image formats.

The software provides wizard-based run setup and convenient analysis and template profiles for standardized sample processing, and offers effortless, customizable documentation of results.

The QIAxcel ScreenGel software is based on a unique algorithm, that has been proven to analyze separation data more reproducibly and accurately than other chromatographic analysis packages. It calculates a variety of peak properties, such as peak number, peak height, peak width, and peak area.

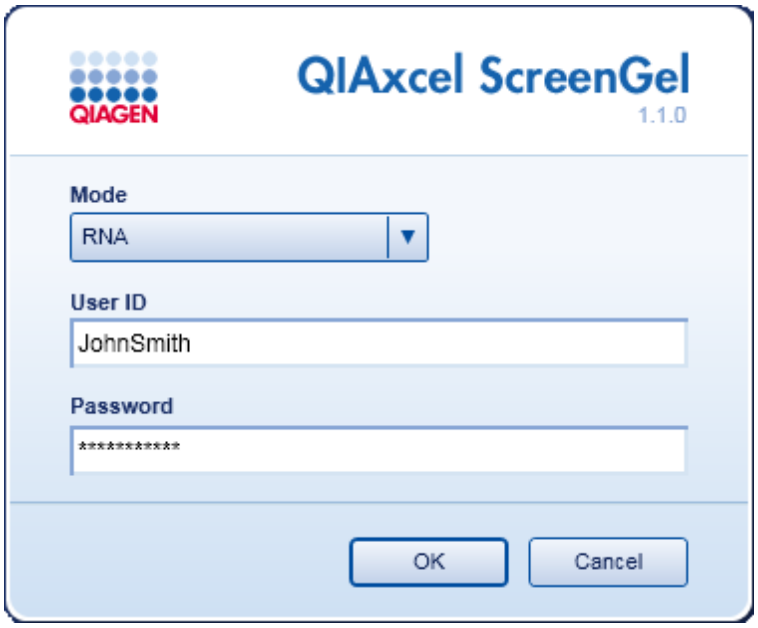
6.1 Concepts

This section explains fundamental concepts that each user working with QIAxcel ScreenGel software should become familiar with:

- Modes
- User management
- Environments
- Profiles
- User interface

6.1.1 Modes

The QIAxcel ScreenGel software currently has three modes — one for DNA, one for RNA, and one for protein analysis. The main purpose of the modes is to adapt the data analysis algorithms to the properties of the analytes. In addition, the modes ensure that valid cartridge types are used and that only data of the right type can be loaded from files.



Mode selection in login dialog box.

6.1.2 User roles

The QIAxcel ScreenGel software distinguishes four different user roles, which differ in permissions. Each user is assigned one of these four user roles. This section provides a short overview of the use and permissions of each user role:

Role	Used for	Tasks	Access
Administrator	User management Software configuration	Installation of software Configuration of global settings Administration of user accounts	Configuration environment
Routine User	Routine sample processing and data viewing	Sample processing Inspecting samples	All environments (restricted access)
Basic User	Sample processing and analysis of data without the option of modifying profiles	Sample processing Analysis of samples Report/export	All environments (restricted access)
Advanced User	Sample processing Analysis of data with full access to analysis parameters Creation and modificationof profiles	Creating/modifying profiles Sample processing Analysis of samples Report/export	All environments (full access)

- Administrator
  This role is intended for management of settings and users.
  Users assigned this role can change the global settings and perform user management, i.e., management of user accounts (rights, user role, etc.). Users do not have access to profiles, the "Process" environment, the "Analysis" environment, or the "Service" environment.
  Handover to a user with the user role "Administrator is possible.
- Advanced User
  This role is intended for experienced users.
  Users assigned this role have access to the full functionality of the software, except for user management. Users can create analysis, process, and report profiles and therefore prepare the working base for other users. They can perform advanced analyses, such as comparison of results from different processes (see Customizing experiments) and modify profile parameters, if required.
  This role is recommended for users working in protein mode.
  Handover to a user with the user role "Advanced" is possible.
- Basic User
  This role ensures the use of predefined profiles, particularly analysis profiles.
  Users assigned this role have access to all environments of the software; however, they can not create new or modify predefined profiles, such as analysis and process profiles. While setting up a new process using predefined process profiles, they can modify marker settings and rows that need to be processed. In the analysis environment, they can open existing experiments and perform routine analyses using predefined analysis profiles, but they cannot modify individual analysis parameters. They can perform report and export using predefined report/export profiles with the option to modify the report/export parameters, but without the option to save this changes.
  Handover to a user with the user role "Basic User" or "Advanced User" role is possible.
- Routine User
  This role is intended for laboratories that routinely process large numbers of samples. Users are guided by a wizard for efficient process setup.
  Users assigned this role are limited to performing processes using predefined process profiles. In the analysis environment, they can open existing experiments for viewing purposes only.
- Handover to a user with the user role "Routine User", "Basic User", or "Advanced User" role is possible.

Note: One person can be assigned several user roles by creating several user accounts with different roles.

Refer to the User management section for information about how to create user accounts.

6.1.3 Environments

The QIAxcel ScreenGel software is composed of four environments providing different functionality. Only one environment can be used at a time.

Environment icons with active "Process" environment.

To switch to an environment, click the environment icon. The functionality of the environments is briefly described in the following table:

Environment enabling runs to be performed on the QIAxcel Advanced system.

Supports data acquisition, allowing integrated data analysis and reporting. For detailed information, refer to the Process section.

Environment that displays and enables analysis of sample data.

Provides advanced visualization and analysis tools for sample data as well as report and export functionality. For detailed information, refer to the Analysis section.

Environment for maintenance or service of the QIAxcel Advanced system.

Contains all functions for maintenance and troubleshooting of instrument and cartridges. For detailed information refer to the Service section.

Environment for administration of users and system configuration.

Provides access to user management, profile management, and software preferences(settings). For detailed information, refer to the Configuration section.

6.1.4 Profiles

Data acquisition and analysis in the QIAxcel ScreenGel software are controlled by so-called "Profiles". Profiles combine settings and parameters and can be conveniently re-used for different purposes (see table below).

The standard procedure is to use predefined profiles. The QIAxcel ScreenGel software will be installed with a set of predefined profiles that cannot be modified. If, however, modifications are necessary, experienced users can create new profiles or change profile settings as required. See the following table:

Profile	Description
Process profile	To define settings for data acquisition. Defines all parameters for the electrophoresis run.
Analysis profile	To define the settings for sample data analysis (analysis parameters).
Peak calling instruction	To define search criteria for peaks of interest.
Report/export profile	To define report and export of sample data and analysis results in various formats.

Note: Process profiles can include an "Analysis profile", a "Peak Calling Instruction", and a "Report/ Export profile", which allows fully automated processing including analysis and report.

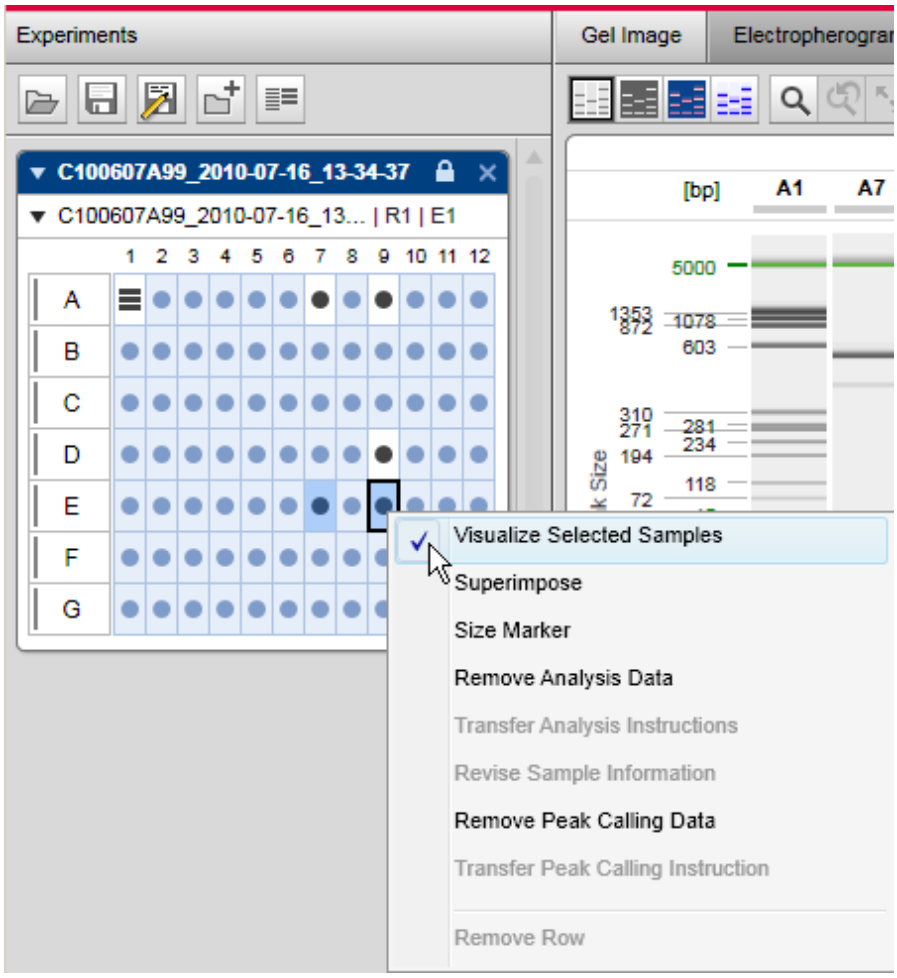
Note: Analysis and report/export profiles and peak calling instructions are included in a process profile by copying the profile name and all profile parameters into the process profile. That means that modifications to the original profiles are not automatically present in the process profile. This prevents process profiles from being changed by mistake and ensures process stability. If the modifications should also be in the process profile, include the modified profile again.

6.1.5 General software usage

QIAxcel ScreenGel software is a modern software with a state-of-the-art graphical user interface. The controls of the user interface behave in the same way as standard Windows controls. This section explains frequently used terms and several concepts which are specific for the QIAxcel ScreenGel software user interface.

In the following table, user interface-related terms that are used in this manual are explained.

Left-click	Press the left button of a computer mouse or touchpad.
Right-click	Press the right button of a computer mouse or touchpad.
Double-click	Left-click twice, very quickly.
Drag-and-drop	Move an object (sample, lane) to another place using a computer mouse or touchpad. Left-click to pick up the object. Hold the left mouse button pressed while dragging the object to the new place. Release the mouse button to release the object in its new position. If more than one object was selected, the left-click picks up all selected objects.
Context menu	When right-clicking certain controls, a context-sensitive menu is shown. Not all controls provide a context menu.



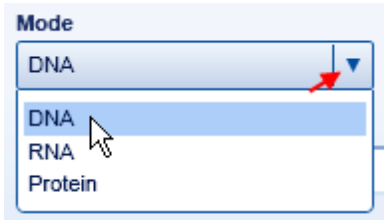
Context menu in the "Experiment Explorer".

Tool tip

When the mouse pointer hovers over a control without clicking it, a small text window appears. Not all controls provide a tool tip. Usually a tool tip gives useful information about the functionality of a control, or useful information about possible problems (errors or warnings).

Drop-down box

Drop-down lists allow the selection of one item from a predefined list of items. First, left-click on the triangle to open the list. Then move the mouse down to the correct item. Left-click to select the item.



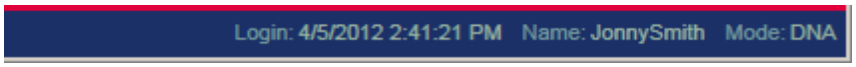
Drop-down box example.

Toggle button

Left-click the button to toggle. When the button is pressed, the functionality is "on". Left-click the the button again to toggle the functionality "off".

"Rubber band" function	Span a "rubber band" to define a rectangle region (for zooming into). Left-click to define the starting point, hold the mouse button pressed while dragging. While dragging, a "rubber band" is shown, spanning around the rectangle region. Release the mouse button to define the region. The "rubber band" disappears. The system performs the (zooming) functionality based on the defined region.

The status bar (the information line at the bottom of the application window) shows the current user logged in, the date and time, user login name, and application mode (DNA, RNA, or protein).

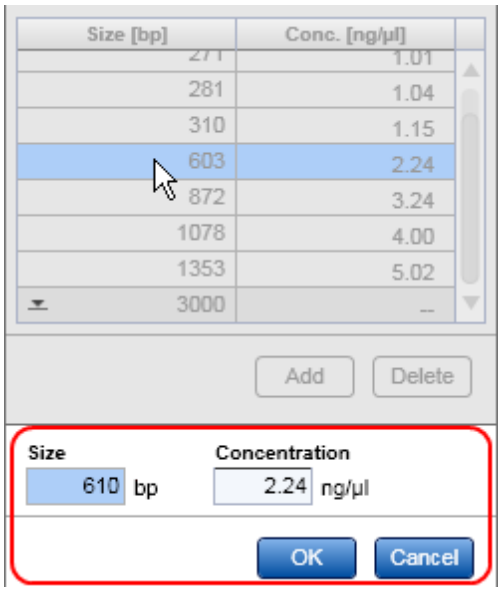


Status bar

6.1.5.1 Editing data in tables

The graphical user interface of QIAxcel ScreenGel contains many tables. When the table data is editable, this can be performed in a special edit area at the bottom of the table. The table cells themselves are not editable.

An example of an editable table is a Size Marker table in the "Process" environment.



Special area for editing table contents.

For example, to change the base pair size from 603 to 610:

1. Highlight the required row by left-clicking it.
2. Click on the "Size" edit field below the table.
3. Enter *610*.
   While editing, only the controls of the edit area are enabled. In this case the edit fields "Size" and "Concentration" are enabled and also the buttons "OK" and "Cancel".
4. To accept the values into the "Size" and "Concentration" fields, click "OK".
   To cancel editing and discard the changes click "Cancel".

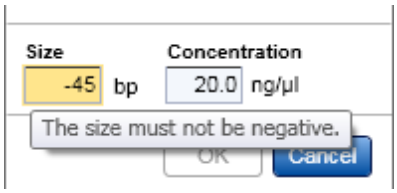
Note: The "OK" and "Cancel" buttons are only enabled if the values in the editable fields have been changed and are valid.

6.1.5.2 Displaying errors and warnings

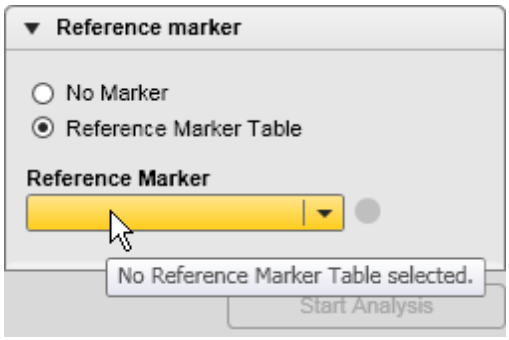
In QIAxcel ScreenGel, yellow controls indicate an error, a warning, or an inconsistency or incompleteness in entered data.

Validation during editing

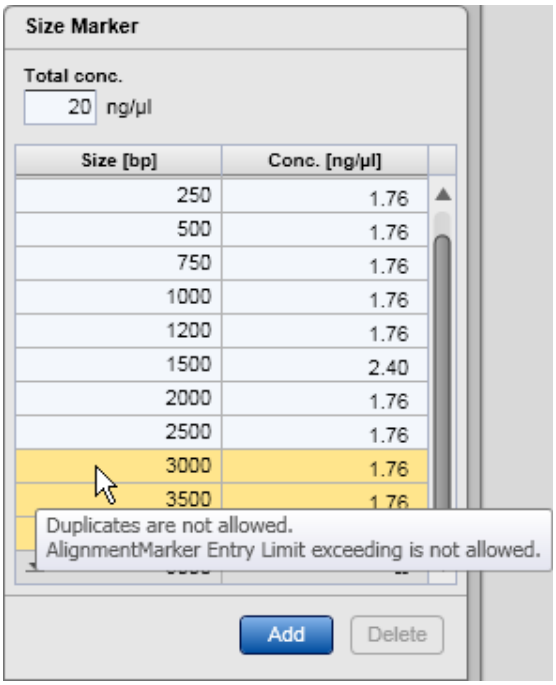
If an incorrect value is entered into an editable field, the background becomes yellow. In addition, a tool tip will be displayed which explains the problem. The following screenshots show examples of errors and the corresponding tool tips.



Negative numbers are not allowed.



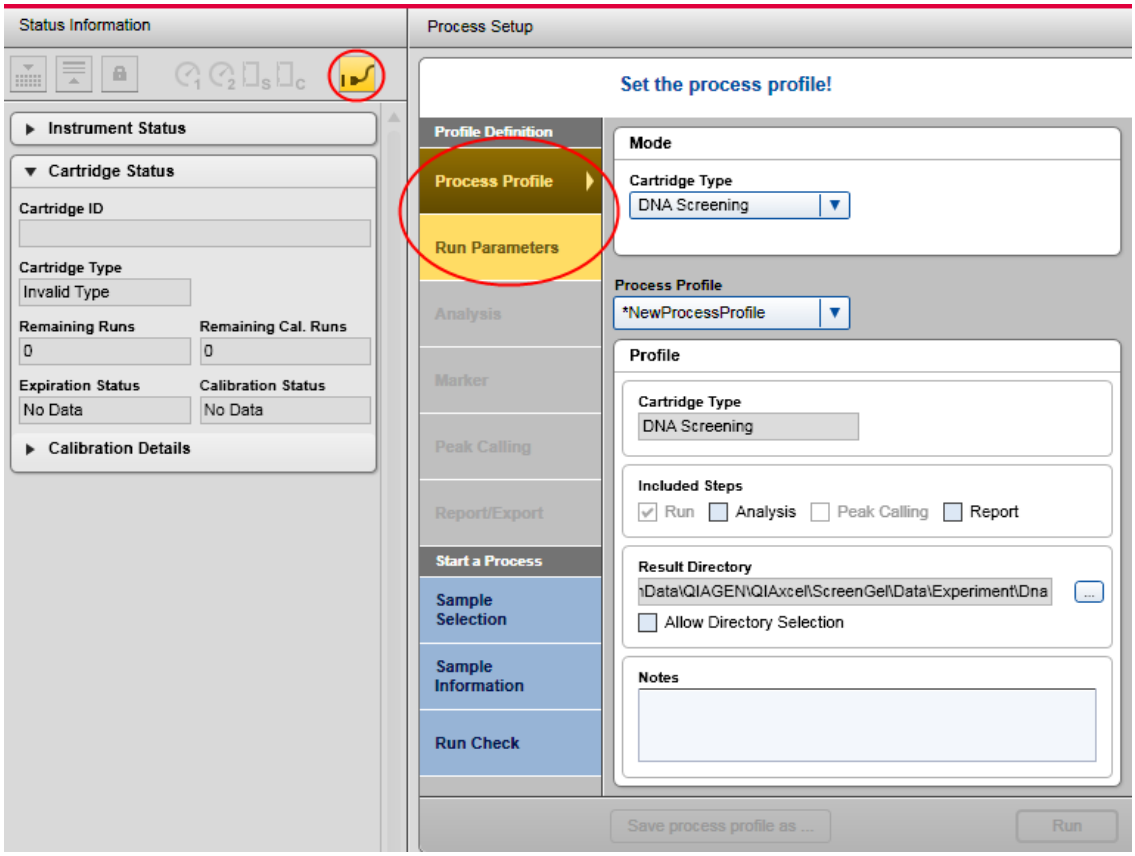
You must select an item.



1. Duplicate entries are not allowed.
2. Exceeding the range of the Alignment Marker is not allowed.

Process screens

If a "Process" wizard screen contains an error or a warning, its screen marker background becomes yellow. You should check the data in this screen and correct the problem.

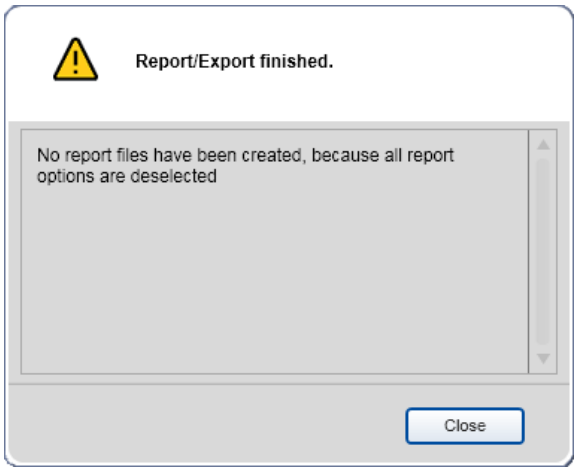


"Run Parameters" screen is incomplete and therefore the process profile is invalid. Additionally, the instrument is not connected.

Note: The screen marker "Run Check" remains blue (normal state) even if errors/warnings have been detected. To start a process, operate as described in the Running procedure section for routine users or the Running a process with advanced options section.

Message boxes

Most problems in QIAxcel ScreenGel are reported using message boxes.



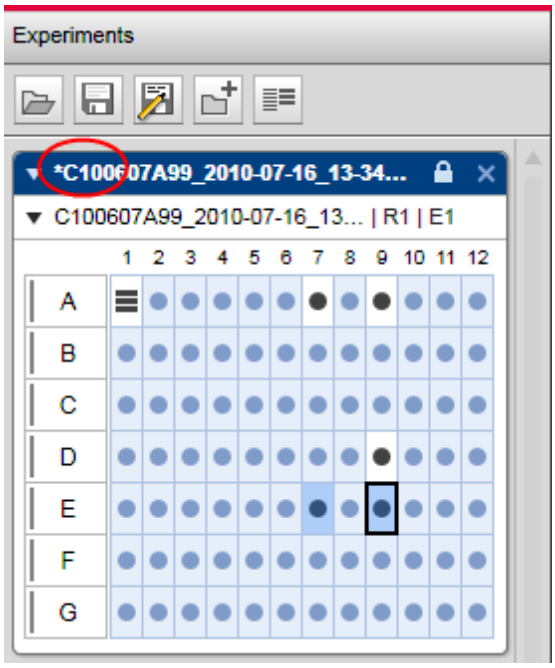
Error message box.

6.1.5.3 Displaying modifications

The QIAxcel ScreenGel displays modifications in a Windows compliant way, using an asterisk at the left of the name of the modified object. This is demonstrated by a few examples.

"Analysis" environment/modification of an experiment (apply or remove analysis, change the lane order, etc.)

The name of the experiment will be displayed with an asterisk.

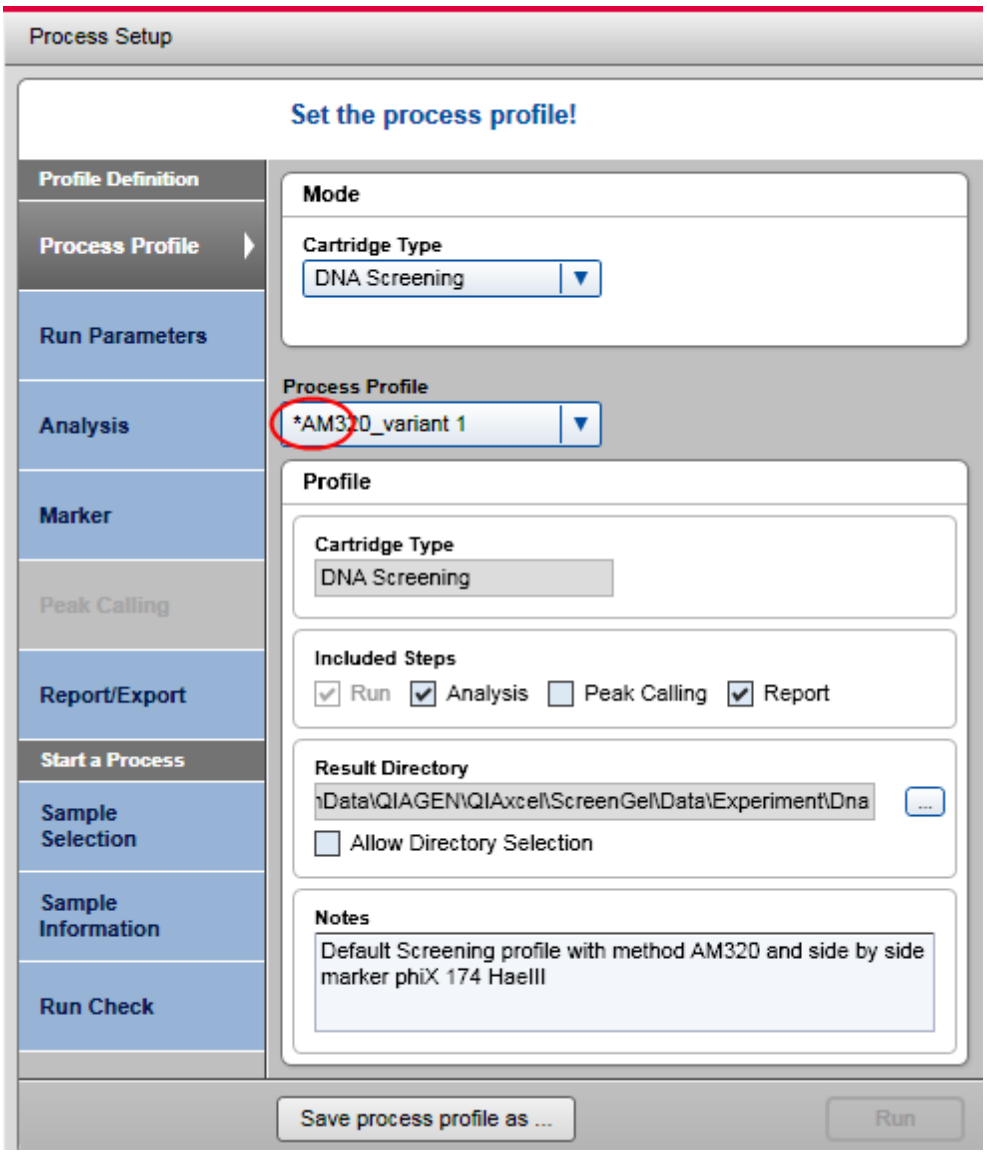


Modified experiment.

Note: A changed profile will be shown in the same way.

"Process" environment/change of any parameter in the "Process" wizard

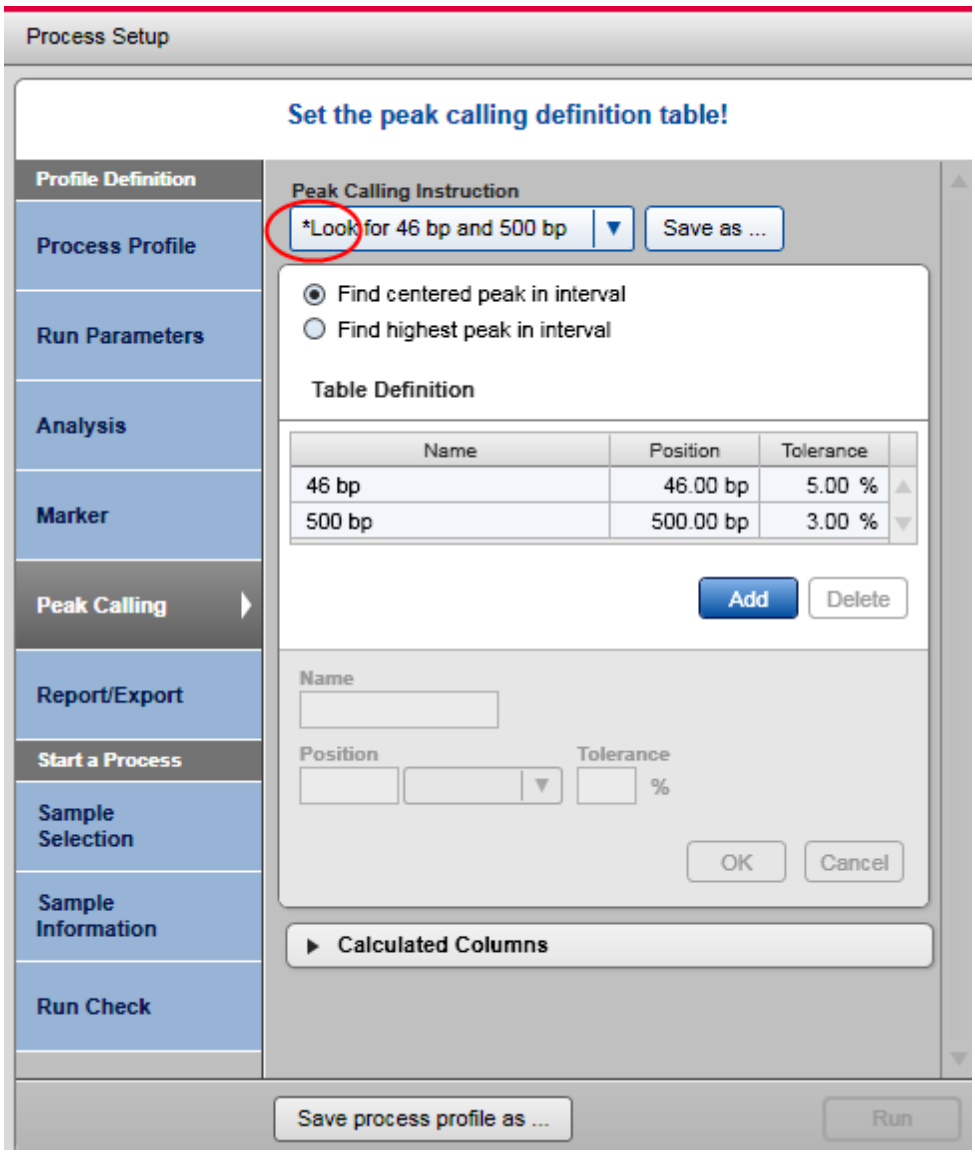
The selected process profile will be displayed with an asterisk.



Modified process profile.

Change of parameters in the "Peak Calling" screen

The selected peak calling instruction in the "Peak Calling Instruction" drop-down list will also be displayed with an asterisk.

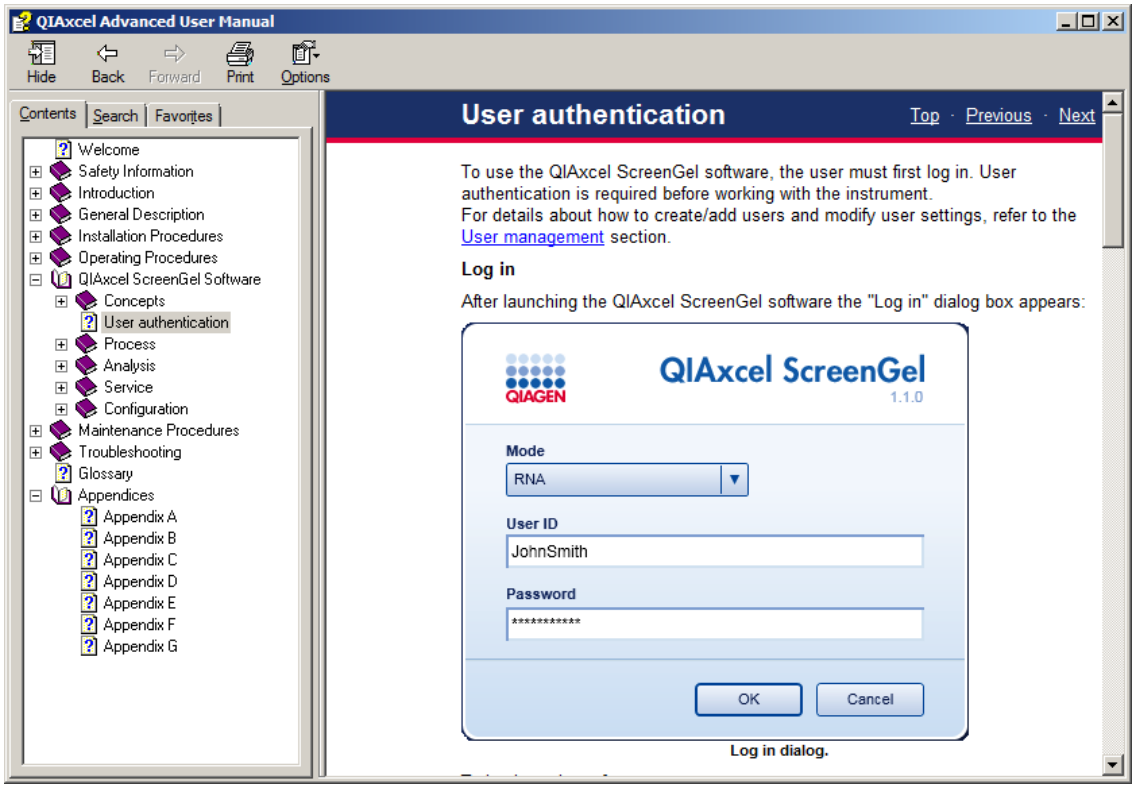


Modified peak calling instruction.

Note: You can start a process or leave the "Process" environment without saving your changes. QIAxcel ScreenGel software will not remind you to save a process profile as well as the corresponding analysis profile, report/export profile, or peak calling instruction. If you leave the "Process" environment, log out, or exit the application, you should save your changes if they are to be reused.

6.1.5.4 Getting help

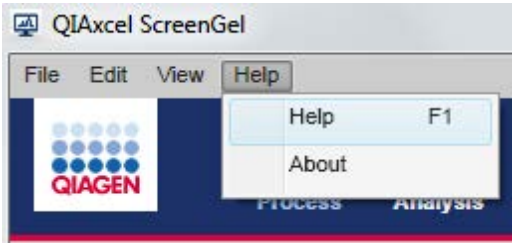
The QIAxcel ScreenGel software has a context-sensitive help system. After pressing the **F1** key, a context-specific help page is shown. The following image shows the help page corresponding to the login screen:



Help page shown after pressing the F1 key while in the login screen.

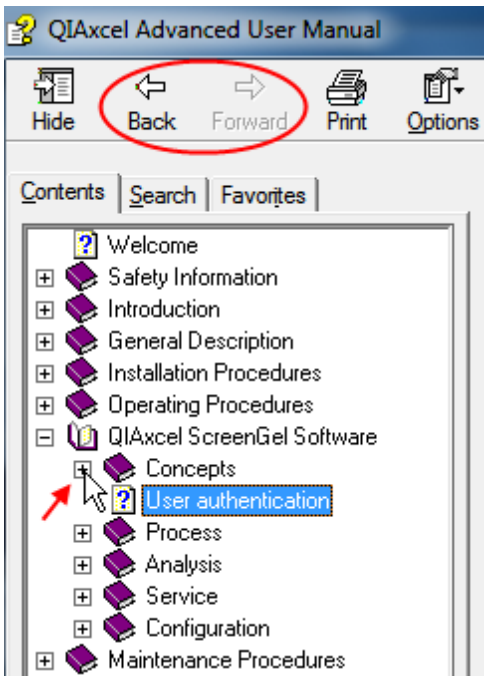
Note: The start menu folder under "QIAGEN"/"QIAxcel" also contains links to the user manual in PDF and CHM format.

Alternatively, select "Help" from the "Help" menu.



Access help from the "Help" menu

Find a description of the software features in the section QIAxcel ScreenGel Software, organized into sections corresponding to the environments of the software, respectively. Use the content tree on the left-hand side to navigate through the help system.



Click to expand the content tree.

The help system provides several links to other sections. Use the navigation links or buttons of the help system to return to the previous topic.

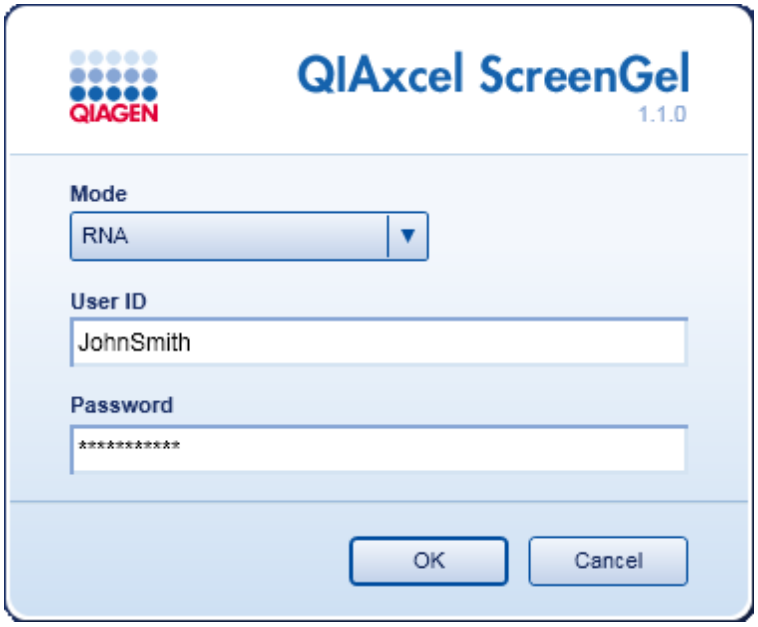
Click to navigate back.

6.2 User authentication

To use the QIAxcel ScreenGel software, the user must first log in. User authentication is required before working with the instrument.
For details about how to create/add users and modify user settings, refer to the User management section.

Log in

After launching the QIAxcel ScreenGel software the "Log in" dialog box appears:



Log in dialog.

To log in to the software:

1. Select the application mode (DNA, RNA, or protein mode).
2. Enter the User ID.
3. Enter the password.
4. Click "OK".

Note: The mode last used is preselected in the "Mode" drop-down list.

Note: To change the mode, log out and then log back in again, or restart the application.

Note: If 21 CFR Part 11 support is activated in the Settings and "Maximum number of failed logins" is set, the number of failed login attempts is limited. If the limit of failed login attempts is exceeded, the user account is locked. The administrator can unlock the user account in the user manager. If the administrator account is locked, please contact QIAGEN Technical Services.

Note: Refer to the User management section for information on how to create user accounts.

Note: Refer to the Getting started with the QIAxcel ScreenGel software section for information on the first login.

Log out

To log out:

1. Select "File"/"Logout" from the application menu bar.
2. A dialog box appears that asks whether you really want to log out. Click the "Yes" the button to confirm the log out.
3. After logging out, the log in dialog box appears.

Note: If you want to exit the QIAxcel ScreenGel software, cancel the log in dialog box first.

Hand over

The user can hand over the current session to another user. Hand over is particularly useful as the current working environment, including all open experiments, can be transferred to a different user with equal or extended user rights, e.g., for changing a shift, or advanced analysis, or maintenance.

Note: A handover can only be made to users with an equal or higher user role.

To hand over:

1. Select "File"/"Handover..." from the application menu bar.
2. The "Hand over" dialog box appears.
3. Enter the User ID and password and click "OK".

Changing the user password

To change your password:

1. Select "File"/"Change Password..." from the application menu bar.
2. The "Change password" dialog box is displayed.
3. Enter the old password.
4. Enter the new password.

   Note: The password must contain one upper-case character, one lower-case character, and one digit. The minimum size of the password is eight characters.
5. Confirm the new password.
6. Click "OK".

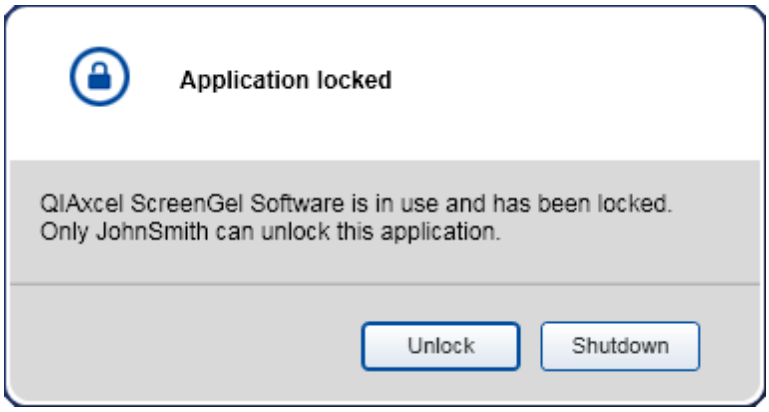
Dialog box that enables the user password to be changed.

Locking the software

The software can be locked to block user access if the computer is left unattended.

To lock the software:

1. Select "File"/"Lock Application" from the application menu bar.
2. When the application is locked, the following dialog box is shown:


Application locked
QIAxcel ScreenGel Software is in use and has been locked.
Only JohnSmith can unlock this application.
Unlock
Shutdown

Dialog box that enables the application to be unlocked.

Automatic software lock

In order to support 21 CFR Part 11 requirements, the software can be automatically locked after a defined time without user interaction. You can activate 21 CFR Part 11 support and specify the auto-lock time period in the Settings. For further details, refer to the Settings section.

Unlocking the software

To unlock the software:

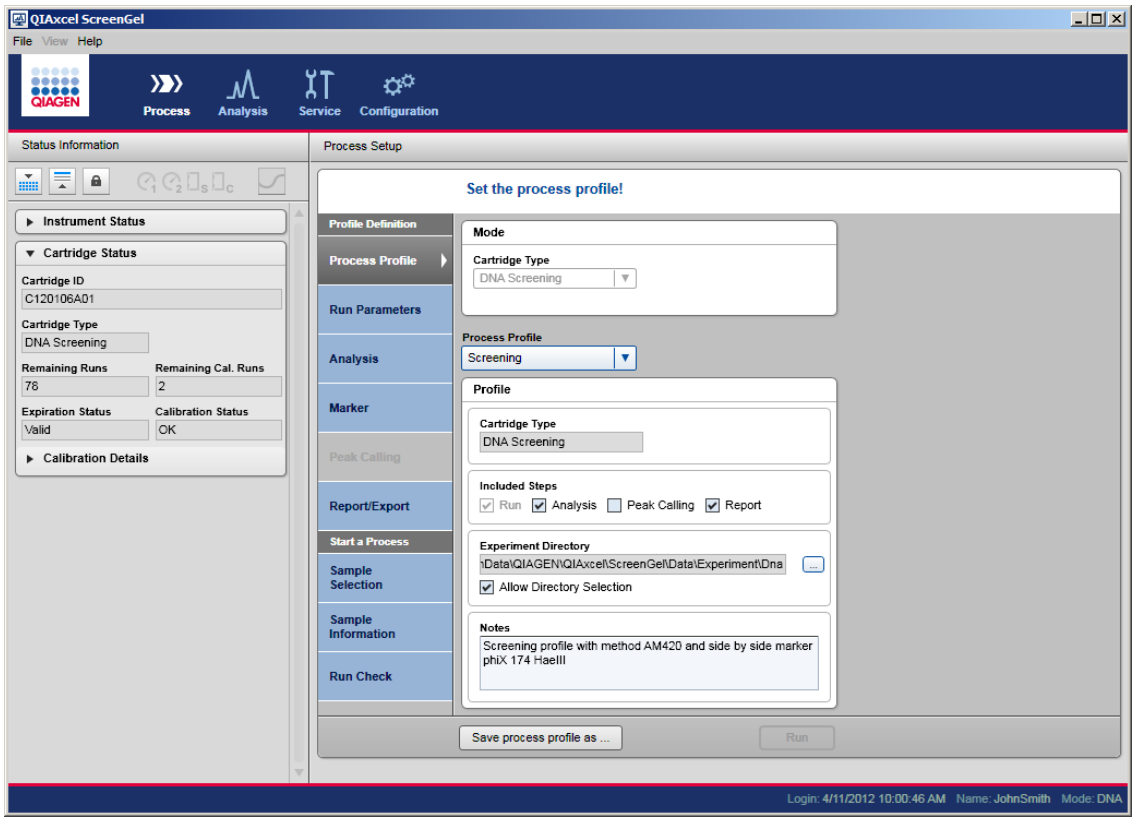
1. Click the "Unlock" button.
2. The Log in dialog box is displayed.
3. Enter User ID and password, click "OK".

Note: Only a user with an equal or higher user role can unlock the application.

6.3 Process

The "Process" environment provides all functionality required for data acquisition:

- Defines process parameters
- Starts the sample process
- Observes the data acquisition process



"Process" environment with active "Process Profile" screen and "Status Information" panel to the left (Advanced User view).

The parameters for the process can be stored for re-use in a process profile.

Refer to the Starting a run section for information about how to start data acquisition using a predefined process profile. This means that all parameters for data acquisition and also for analysis and report are already defined. The specific sample information has to be entered and the process started. This can be performed by users with the assigned user roles "Routine User", "Basic User", or "Advanced User".

Refer to the Running a process with advanced options section for detailed information about how to define process parameters and to start a process. This requires the user roles "Basic User" or "Advanced User"; however, there are some limitations for users with the user role "Basic User" with respect to analysis parameters and methods.

To fully automate a process, define a process profile that optionally includes an "Analysis" profile for analysis parameters and marker information, as well as a peak calling instruction, and a "Report" profile for report/export parameters. Refer to the Creating a new process profile and Modifying a process profile sections for information on how to prepare and save process profiles for reuse. This requires the user role "Advanced User".

The data acquired during processing will be stored in an experiment. Refer to the Run parameters and result structure and Handling samples and experiments sections for detailed information.

6.3.1 Running a process with advanced options

Users with the assigned user role "Advanced User" or "Basic User" can modify process profiles, if required. Restrictions apply to users with the role "Basic User" as they can, for example, start a modified process profile, but cannot save it. Restrictions are annotated, where they apply.

Note: For information about how to start a process as a user with assigned role "Routine User" refer to section Starting a run.

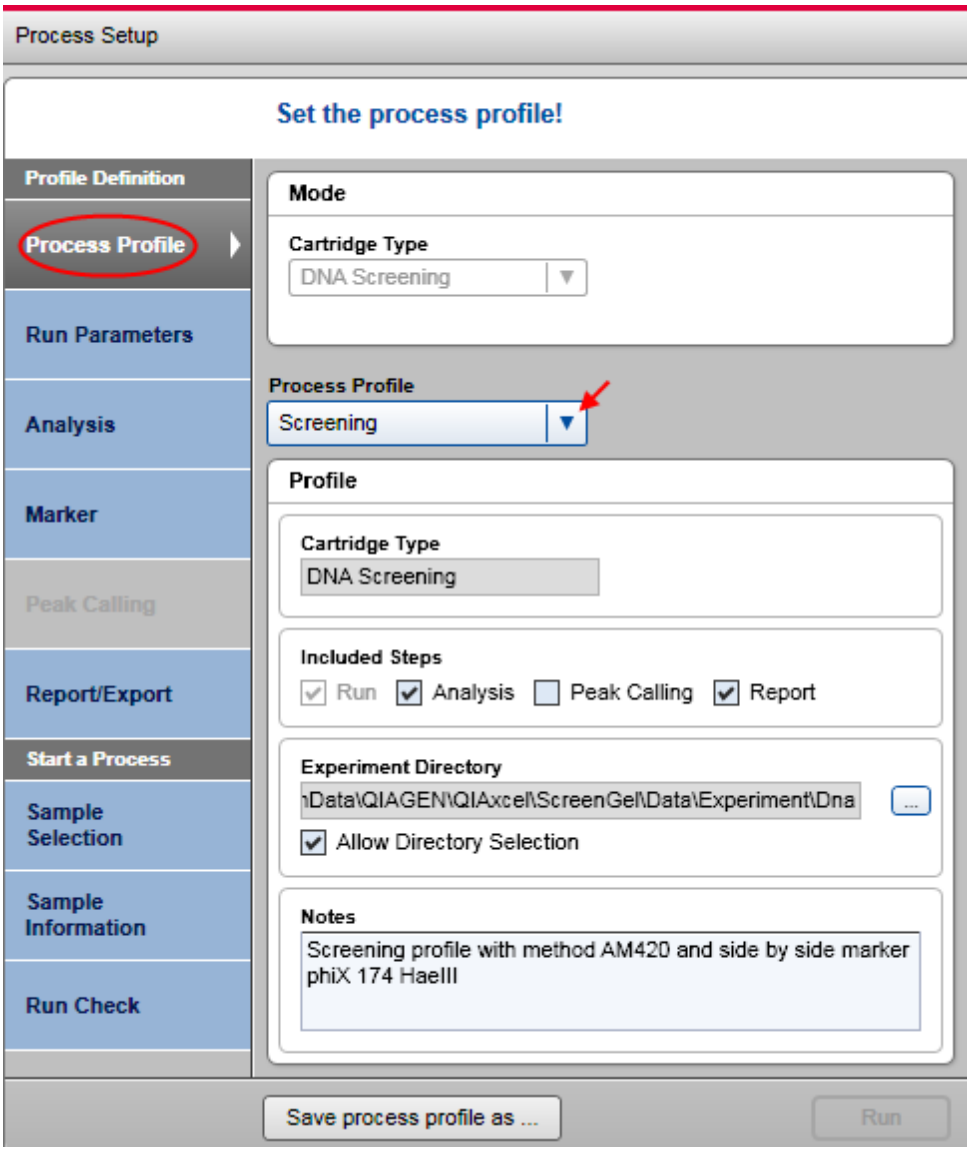
Follow these steps to perform runs with advanced options:

1. Switch on the QIAxcel Advanced at the power switch.
2. Switch on the computer, launch the QIAxcel ScreenGel software from the Windows start menu under "QIAGEN/QIAxcel" or from the desktop icon.
3. In the QIAxcel ScreenGel software, select a mode (DNA, RNA, or protein) and log in (for detailed information refer to the User authentication section). The "Process" environment opens and displays the first screen of the process profile of the process wizard.

   Note: The icon indicates that the connection is being established and the icon shows that the QIAxcel Advanced is connected.
4. Install the QIAxcel gel cartridge to be used as described in Installing a QIAxcel Gel Cartridge and smart key.

   Note: You can inspect the cartridge status in the "Status Information" panel to the left of the "Process" environment. Refer to the "Status Information" panel section for detailed information.
5. Place the buffer tray containing the QX Alignment Marker onto the buffer tray holder as described in Loading the buffer tray.
6. Place the sample strips (in position A) or a 96-well plate onto the sample plate holder.
7. Close the sample door.

   Note: If the instrument doors are closed, the buffer tray automatically moves to the "Wash park" position after a period of 5 minutes.
8. In the "Process" environment of QIAxcel ScreenGel, select a process profile in the "Process Profile" screen.



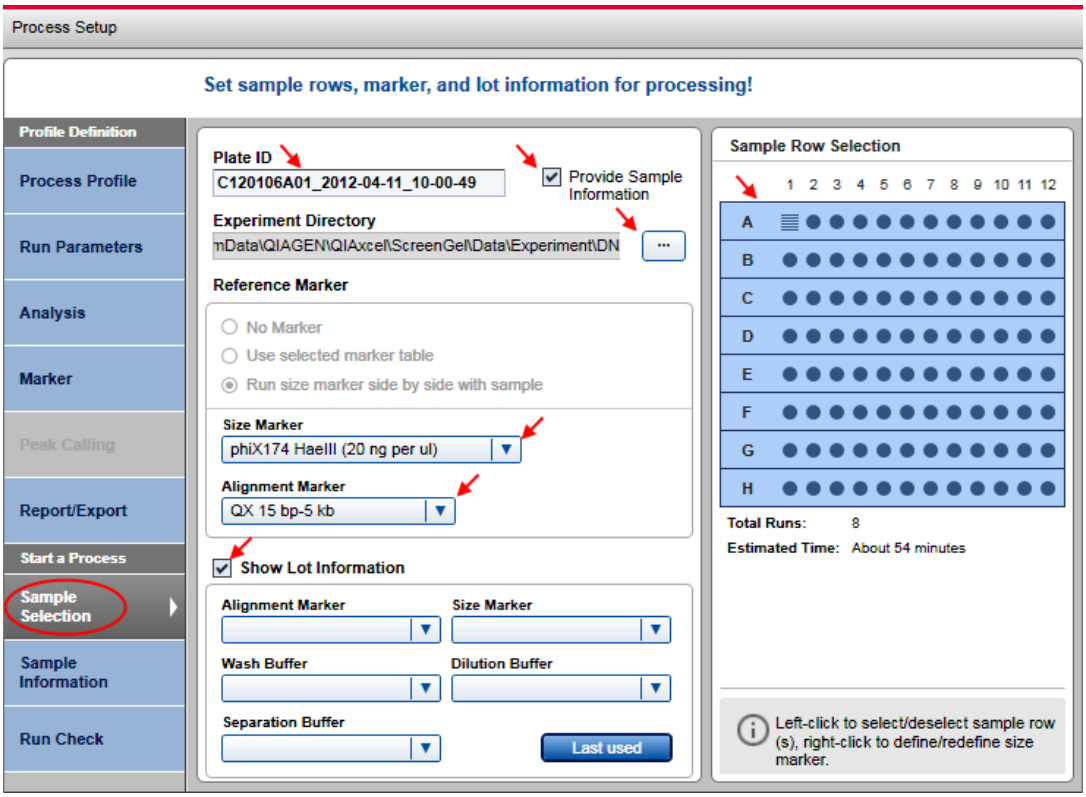
"Process Profile" screen with "Screening" profile selected.

Note: Select "NewProcessProfile" to create a process profile from scratch. The system will show "NewProcessProfile" after selection. This is only possible for users with the assigned role "Advanced User". However, it may be easier to select a predefined process profile close to your needs and only modify it slightly.

9. **Optional**: Modify the process profile options if required, as described in the Process profile options section; restrictions for "Basic Users" are described here.

   Note: Experiment directory, markers, and sample rows can be adjusted in the "Sample Selection" screen below, if the process profile allows it. As these adjustments override the options defined in the process profile, modify these options in the process profile only if you want to save them for reuse.

10. **Optional**: Switch to the "Sample Selection" screen.



"Sample Selection" screen.

11. **Optional**: Change the plate ID.

    Note: The plate ID will be used to name all the results from this process, for the experiment storing the sample data, as well as for generated report/export files. Therefore, a unique plate ID is required. See Run parameters and result structure for further information.

    Note: For the plate ID, the software allows alpha numeric characters only (this means that brackets, special letters such as ä or µ, and special characters such as /&!%$§ ' ´ ` @*+~#=<>|;, etc cannot be used.) The software removes blanks at the start and at the end automatically.

    Note: After the process, the plate ID cannot be modified.

    Note: If the settings option "Generate plate ID" is selected, the system automatically generates a plate ID following the rules specified in the settings. Refer to section Settings for more information. However, the plate ID may be modified.

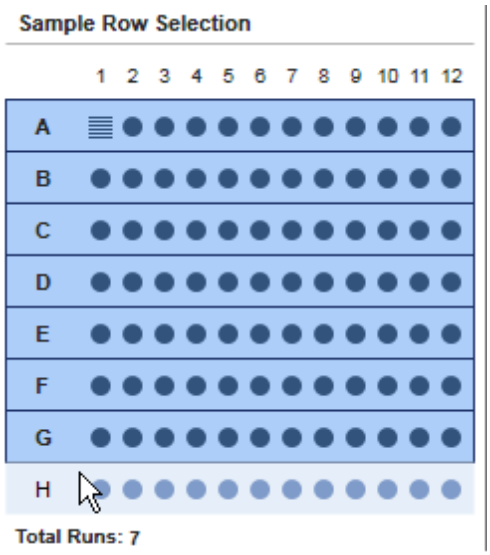
12. **Optional:** Adjust the directory where the experiment will be saved.

    Note: This can be a directory on the network. However, during the process, the experiment will be always saved to a local directory first (refer to Settings), and then copied to the experiment directory defined here, when the process finished.

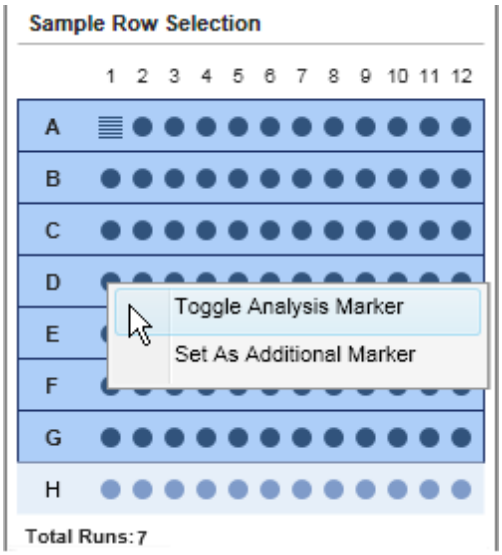
    Note: Changing the experiment directory here is only possible if the process profile allows it (see Selecting general process options); however, you can switch to the "Process Profile" screen to modify this.

13. **Optional**: Change the selection of sample rows to be processed. Use this option if you want to process less rows than specified in the "Run Parameters" screen. Left-click the row to deselect/ select.

Optional: Change the position of the size marker on the plate, by right-clicking the new marker position. Select the option "Toggle Analysis Marker" from the context menu that appears. This size marker will be used for automatic analysis during processing, if analysis is included in the process profile.



Sample row H was deselected.



Changing the size marker position to D1.

Note: Changing sample rows or size marker position here is only possible if the process profile allows it (see Selecting run parameters); however, you can switch to the "Run Parameters" screen to modify this.

Note: It is not possible to deselect a row containing the size marker.

Optional: If you have an additional size marker in the sample plate, right-click the position and select the "Set As Additional Marker" option from the appearing context menu. A rotated ladder symbol appears. Right-click it again and select the "Size Marker Name" from the context menu. This information can be used for manual analysis, but will not be used for automated analysis during processing.

14. **Optional**: Select the size and alignment marker in the "Size marker" and "Alignment Marker" drop-down lists as required. This information will be used for automated analysis during the process.

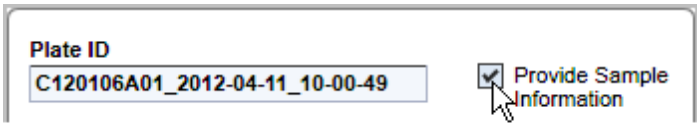
    Note: If the "No marker" option is selected, select the prepared alignment marker. If you do not select an alignment marker in the "Alignment Marker" drop-down list, you will have to acknowledge a warning later in the "Run check" screen.

15. **Optional**: Provide lot information of buffers and markers by checking the "Show Lot Information" box.

    Up to five last-used lot information are stored separately for each lot type. These lastly used values can be selected from drop-down list to use them again. Alternatively, the lot numbers can be typed into the edit field of the combo box. Restore the last used combination of the lot information by clicking on the button "Last used".

    Note: This option is available only if either the option "Enable input fields for Buffer lot IDs" or "... Marker lot IDs" is selected in the settings (see Settings).

16. **Optional**: Check the "Provide Sample Information" box if you want to provide sample information. If not, proceed to step 18.

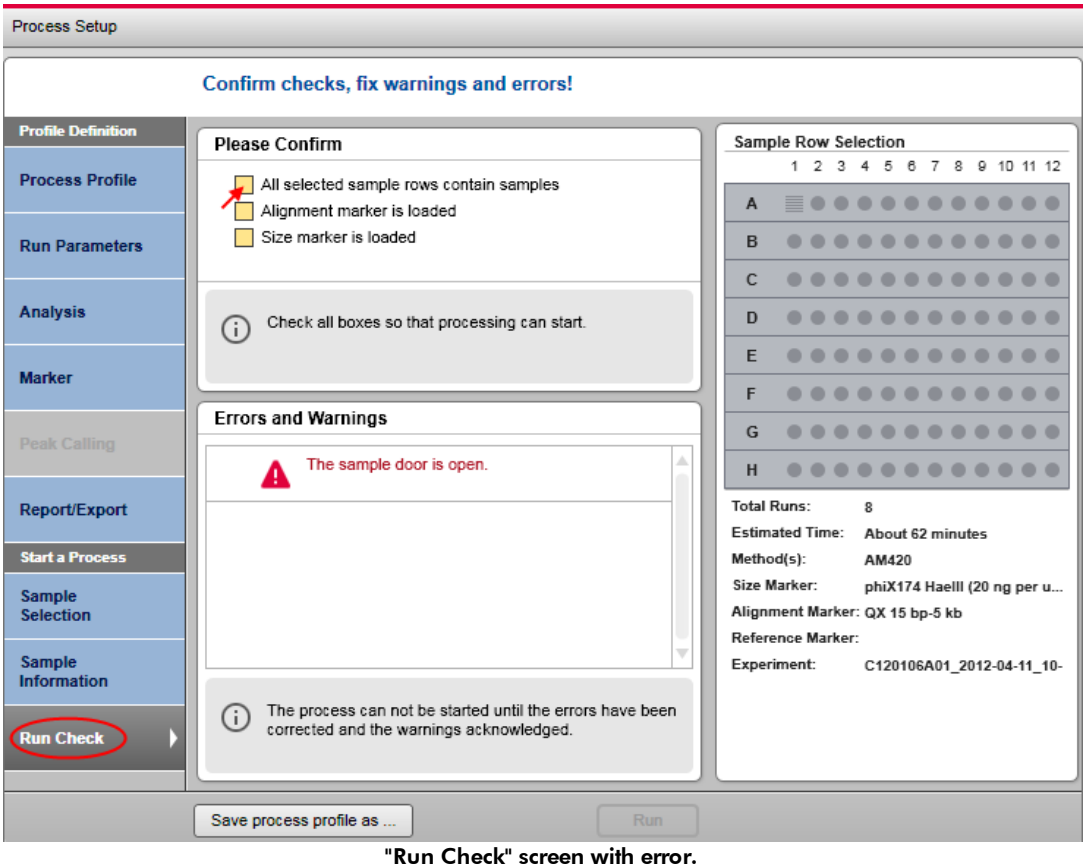


"Provide Sample Information" box checked.

17. **Optional**: Provide sample information in the "Sample Information" screen, entered manually or imported from a file, as described in the section Provide Sample Information.

Note: The "Provide Sample Information" box must be checked in the "Sample Selection" screen to access this screen.

18. Switch to the "Run Check" screen. Confirm all check boxes. Resolve the problems indicated by warnings and errors.



"Run Check" screen with error.

Note: The process can be started only when all run checks are confirmed and no errors are shown. Warnings must be checked as well or removed by eliminating the cause of the warnings.

Note: "Advanced Users" can acknowledge an uncalibrated cartridge and a "red" marked reference marker ("Basic Users" can acknowledge a "yellow" one).

Note: If the run button is still deactivated, check the "Status Information" panel for cartridge and instrument status.

19. Start the process by clicking the "Run" button.

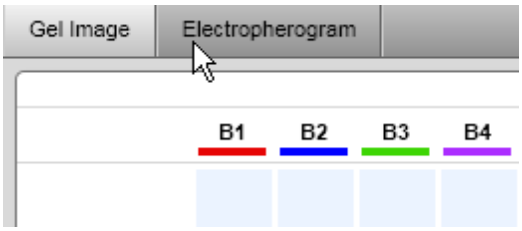
    The process wizard will be closed and a preview will be shown for each row currently processed. The actions performed by the instrument are shown in the "Instrument Status" panel on the left. A progress bar below the preview shows the progress of the whole process and the estimated remaining process time.

    Depending on the report settings the generated report may be displayed.

    Note: Opening the cartridge door or sample door during operation of the QIAxcel will cause the system to stop the action it is currently performing. The process is stopped and cannot be recovered. No sample data are stored for the row currently processed. Sample data are stored for completed rows only. No analysis, peak calling or report/export is performed. Thus, the stored sample data contain raw data only.

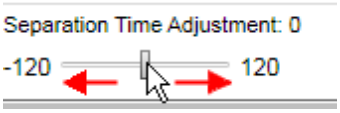
Actions during process run:

- You can switch between the gel and electropherogram preview by clicking the respective tab.



Switching from Gel Image to Electropherogram.

- Optionally adjust the separation time. To do so, move the "Adjust Separation Time" slider below the preview. Moving it to the extreme left position will shorten the separation time by 120 seconds, moving it to the extreme right position will extend the separation time by 120 seconds. Moving the slider takes effect for an actual ongoing separation as well as for all following separations during the process.



Adjust separation time.

Note: The slider can be moved either by using the mouse or by pressing the "Cursor left" or "Cursor right" key on the keyboard.

Note: When starting the next process by clicking the "Run" button, the slider is automatically reset to the middle position and the separation time will be applied as defined in the method.

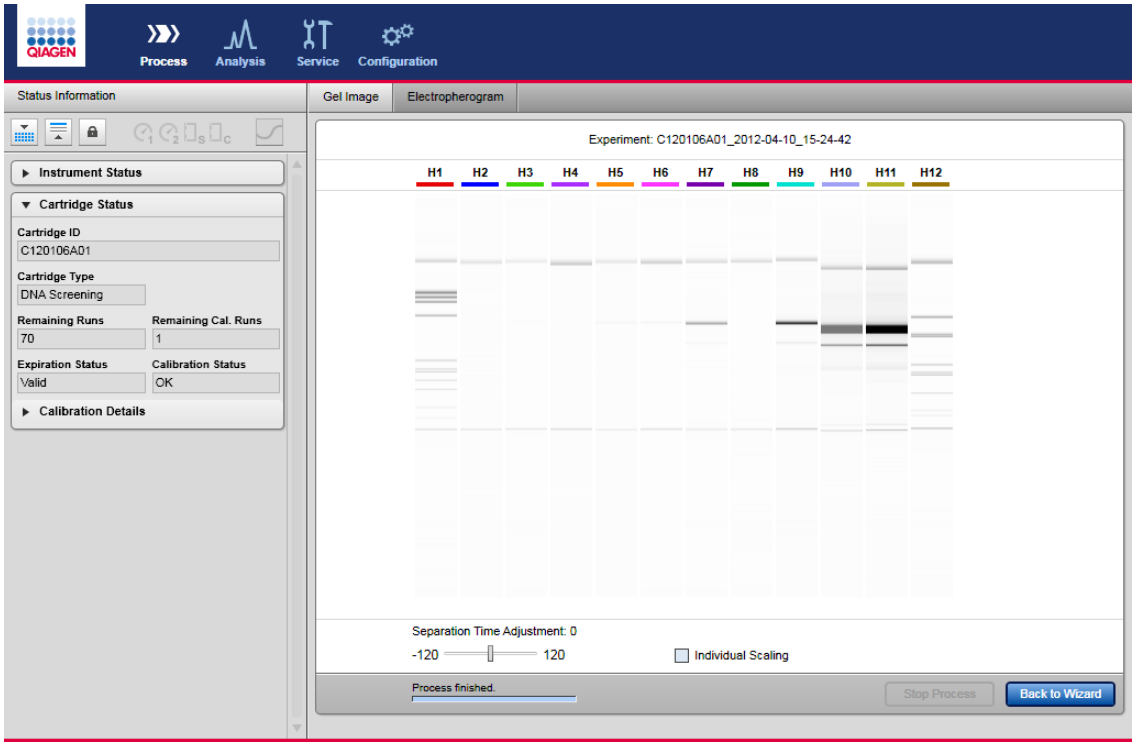
- Optionally switch the check box "Individual Scaling" on/off to adapted colors to the overall maximum signal height of all samples. See Gel view for more information about individual scaling. The check box "Individual Scaling" is off initially.

- The process can be stopped by clicking the "STOP" button below the preview.

  Note: If the instrument motors are currently moving, the process will stop after this movement.

  Note: No sample data are stored for the row processed. Sample data are stored for completed rows only. No analysis, peak calling, or report/export is performed. Thus the stored sample data contain raw data only.

Actions after the process has finished:

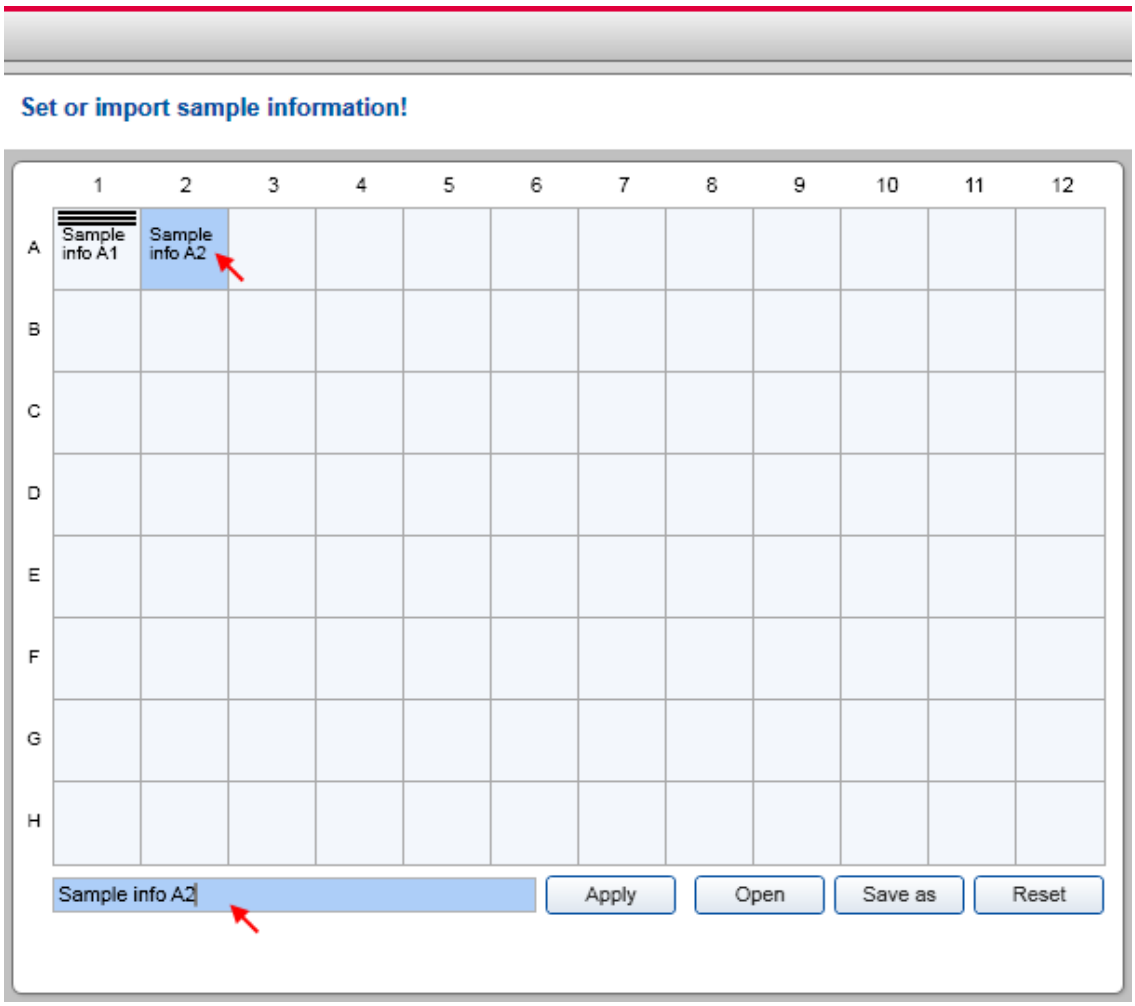


Process has finished.

- The next process can be started by returning to the process wizard, clicking the "Back to Wizard" button below the preview.
- To inspect the sample data switch to the analysis environment. For information how to do that refer to sections Environments, Handling samples and experiments and Viewing sample data respectively. Return to the process environment and click the "Back to Wizard" button to start the next process.

6.3.1.1 Provide Sample Information

As previously mentioned, to access the "Sample Selection" screen, the "Provide Sample Information" check box must be checked in the "Sample Selection" screen.



Entering sample information in the "Sample Information" screen; size marker at A1.

Note: The size marker positions are marked by a "ladder" symbol.

To provide sample information manually, enter the sample information starting at position A1, which is preselected. The entered text is shown in the edit field below the table. Confirm the information for each position by pressing the "Enter" key; the next position will be selected automatically for the next input. To provide sample information for a selected position only, click the position and enter the sample information in the editable field.

To navigate through the sample information grid, use the arrow and "Tab"/"Shift+Tab" keys (just as in a Microsoft® Excel® table).

To select multiple cells:

- Use control-left mouse click to add a cell to selected area or to deselect this cell
- Use the left mouse click and drag to select a rectangular area of cells.

To copy the text of one selected cell into multiple cells:

1. Select the (source) cell.
2. Use the context menu item "Copy" or press the "Ctrl-C" key combination to copy the text into the clipboard.
3. Select the target cells.

4. Use the context menu item "Paste" or press the "Ctrl-V" key combination. The text will be pasted from the clipboard into all selected cells. In addition, the selected cells will remain highlighted after the text has been pasted.

To copy a column:

1. Select all cells of the column you want to copy.
2. Use the context menu item "Copy" to copy the text of all selected cells into clipboard.

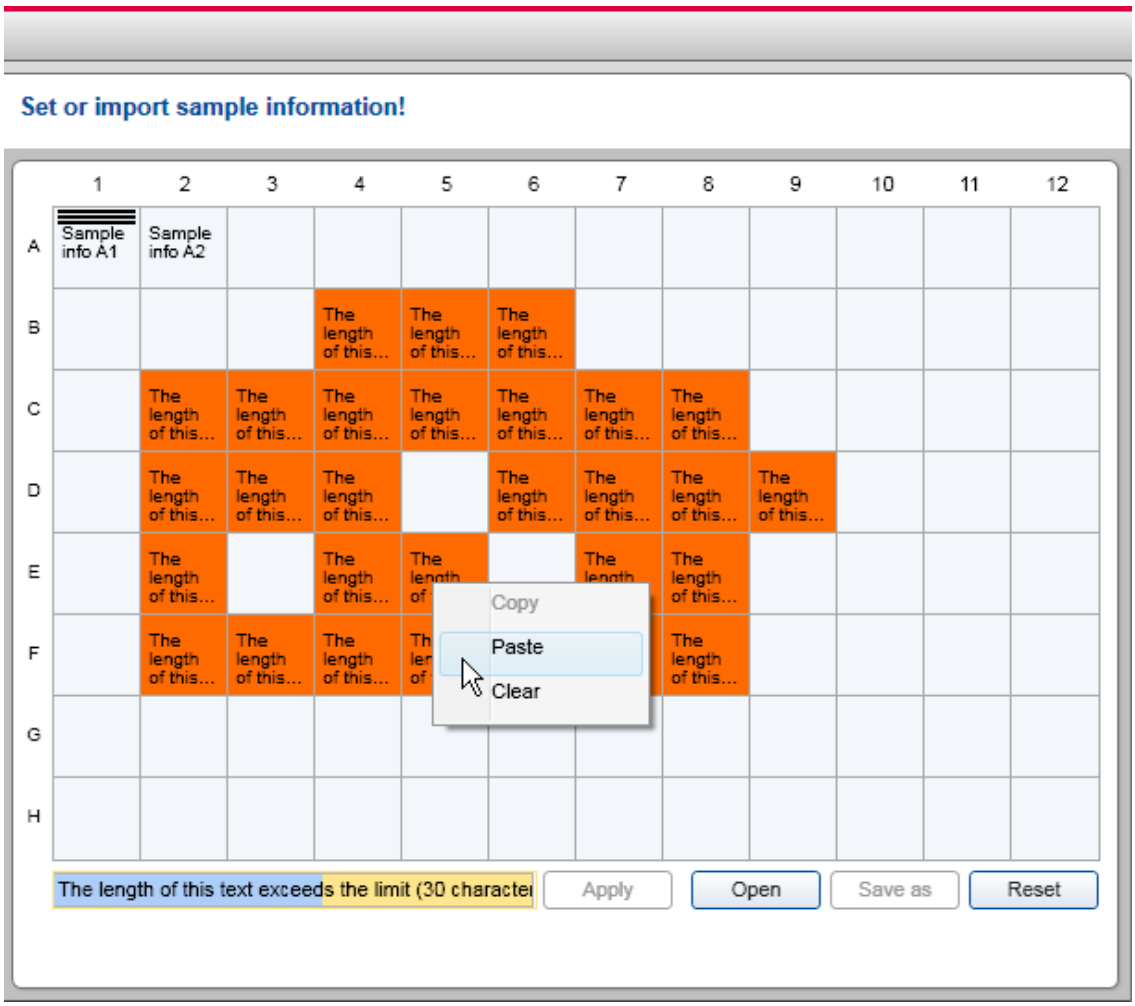
   Note: The "Ctrl-C" key combination captures the text of the last selected cell only.
3. Left-click on the first cell of the column from which you want the text to be pasted.
4. Use the context menu item "Paste" or press the "Ctrl-V" key combination. The cells from the clipboard will be pasted to the column starting with the cell selected in the last step.

Note: In the same way, it is possible to copy rows or other selected areas. To start pasting, click the uppermost cell to the left.

To copy multiple cells from a Microsoft Excel table:

1. Copy the cells from the Microsoft Excel table into the clipboard.
2. In the "Sample Information" screen, click on the most left cell to paste.
3. Use the context menu item "Paste" or press the "Ctrl-V" key combination. The cells from the clipboard will be pasted to the cells starting with the cell selected in the last step.

Note: If the length of the pasted text exceeds the maximum value (30), the cell background will change. The background color of the edit field for a text that is too long is divided in two areas: blue (normal) for the first 30 characters (left-sided) and yellow (erroneous) for the characters that exceed this limit (30), as shown in the figure below. In this case the "Apply" button is disabled. In addition, a tool tip text for the edit field is shown.



Text that is too long (more than 30 characters) that has been pasted into the selected cells.

To save the provided sample information in a file for later reuse, click the "Save as" button. A dialog box will appear listing all the available files. Optionally, navigate to the directory where the sample information will be stored, enter a unique file name, and click "OK".

To import sample information from a file (see the note below), click the "Open..." button. A dialog box will appear listing all available files. Optionally, navigate to the directory where the sample information was stored, select the file and click "OK". The imported data overwrites all sample information previously provided.

Note: Imported sample information is read-only if the settings option "Prevent modification of imported sample information" is selected (see Settings).

Note: It is also possible to import a "rack file" as used in QIAsymphony® and QIAgility® applications. An example can be found in the "Sample Info Import" directory (see Settings).

To clear sample information, use the "Reset" button.

Note: Users who are allowed to revise sample information (see User management) may edit the sample information after the run using the context menu of the experiment explorer. In the analysis environment, select the sample in the experiment explorer, right-click the sample, and select the context menu option "Revise Sample Information", then enter the new sample information.

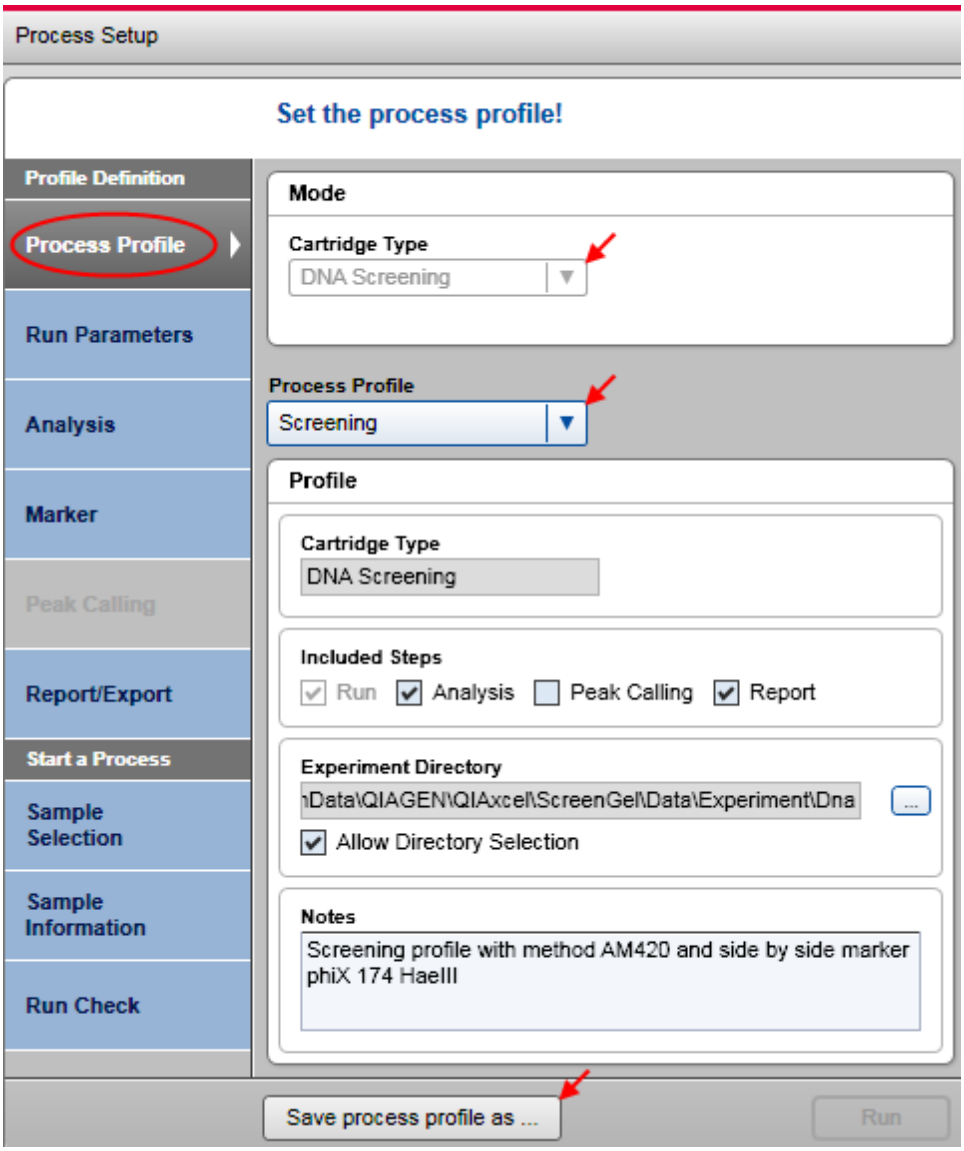
6.3.2 Modifying a process profile

Note: Only users with the assigned role "Advanced User" and "Basic User" can modify process profiles. Restrictions apply to users with the role "Basic User" as they, for example, cannot save the modified process profile. Restrictions are annotated in this manual, where they apply.

To modify a process profile proceed as follows:

1. Launch the "Process" environment.

   If not already open, switch to the "Process" environment by clicking the "Process" environment icon. Select the "Process Profile" screen.



Steps to modify a process profile.

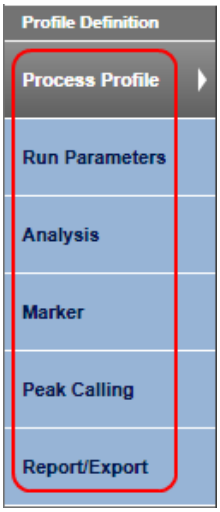
Note: If the last process only just finished, click the "Back to Wizard" button on the right bottom.

2. Select the process profile to be modified.

Use the "Process Profile" drop-down list to select a profile.

Note: Each process profile is related to a certain cartridge type. Therefore, the system can ensure that a process (i.e., data acquisition) can be started only if the correct cartridge type is inserted.
If the process profile you want to select is not listed, make sure that the correct cartridge type is selected. If the instrument is connected, the system automatically detects the inserted cartridge type. If you want to modify a process profile to use with another cartridge type, remove the cartridge, or at least the cartridge key. Select the correct cartridge type. The process profile you want to modify should now be listed in the "Process Profile" drop-down list. Select the process profile and proceed.

3. Change the process profile options as required.



Screens for process profile definition.

See the Process profile options section for detailed information.

4. Save the modified process profile under a new name.

Click the "Save Process Profile as ..." button below the process setup and enter a new unique profile name in the dialog box that appears.

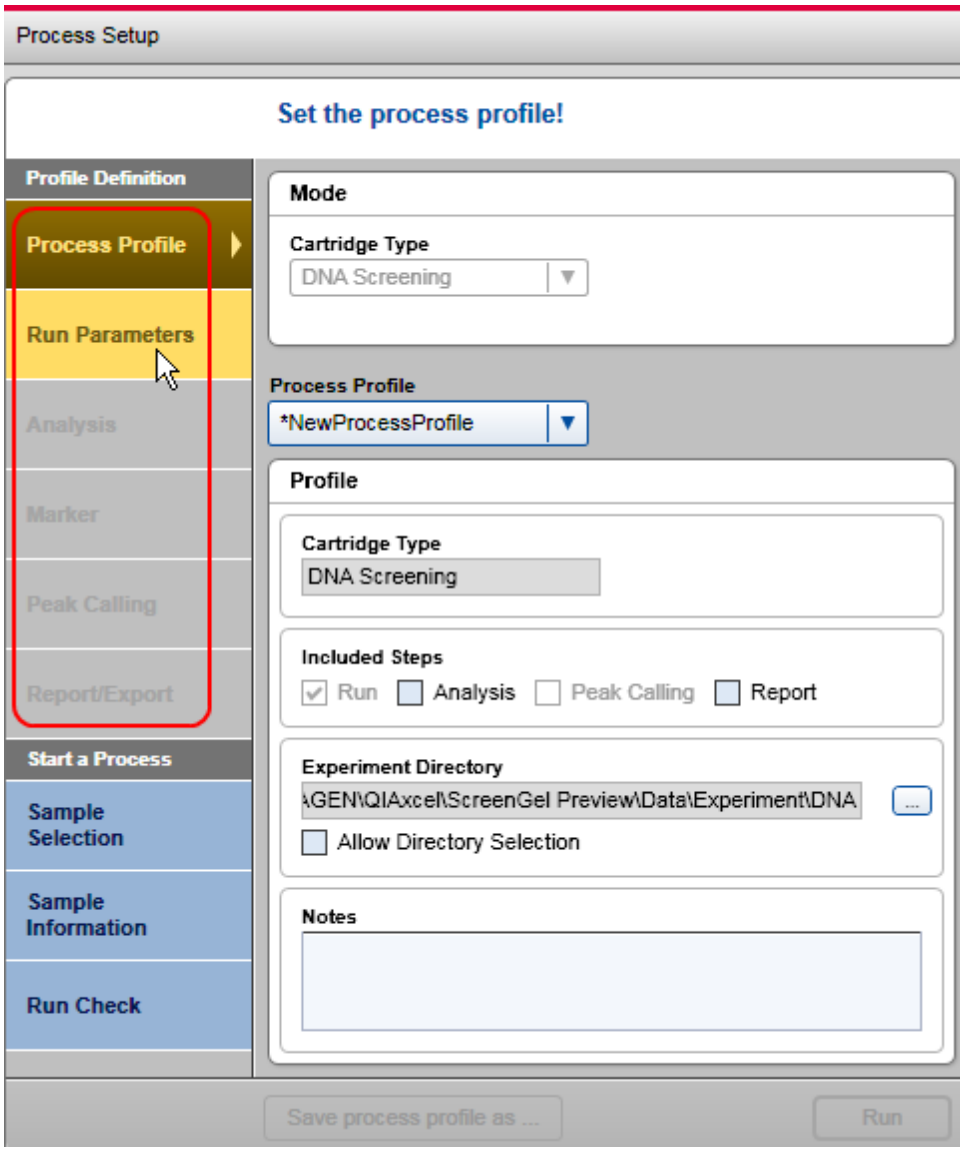
Note: This is possible for users only with the assigned user role "Advanced User".

Note: If there are process profile screens containing incomplete or inconsistent data, which are highlighted in yellow, the "Save process profile as..." button is disabled. Select the marked process profile screens and correct the data. If all data are correct, the "Save process profile as..." button becomes enabled and the process profile can be saved.

Note: You can start a process or leave the "Process" environment without saving your changes. QIAxcel ScreenGel software will not remind you to save a process profile or the embedded analysis profile, report/export profile, or peak calling instruction. If you leave the "Process" environment, log out, or exit the application, you should save your changes if they are to be reused.

6.3.3 Process profile options

The process profile options are grouped into several screens. To specify the complete process profile, follow the screen order as described below. To switch to the "Run Parameters" screen, click the screen name:



Defining a process profile.

Note: You can return to each screen by clicking the screen name. You can skip screens if modifications are not necessary.

Note: Screens with incomplete or incorrect options are highlighted in yellow. There is no need to correct them straight away, but you cannot save or start an incomplete or incorrect process profile.

The "Process Profile" screen options are described below.

Process Profile	Specifies the process scope. In addition to data acquisition, it is possible to include additional steps such as analysis and report. For detailed information refer to the Selecting general process options section.
Run Parameters	Specifies the data acquisition details such as method used, rows to be processed, and size marker position. For detailed information refer to the Selecting run parameters section.
Analysis Parameters	Specifies the analysis parameters for fully automated analysis after data acquisition. For detailed information refer to the Selecting analysis parameters section. **Note**: This screen is disabled if analysis is not in the process scope.
Marker	Specifies the markers, alignment marker, and size marker used for analysis. For detailed information refer to the Selecting marker section. **Note**: This screen is disabled if analysis is not within the process scope.
Peak Calling	Specifies the parameters for peak calling based on the peak result table. For detailed information refer to the Selecting peak calling instructions section. **Note**: This screen is disabled if peak calling is not within the process scope.
Report/Export	Specifies the report and/or export parameters for fully automatic report and export as last step during process. For detailed information refer to the Selecting report/export parameters section. **Note**: This screen is disabled if report/export is not in the process scope.

6.3.3.1 Selecting general process options

1. Select the "Process Profile" screen.

   Refer to the Process profile options screen for information about how to select the screen.

2. Specify the process scope.

   Select the additional steps:

Analysis	Includes analysis in the process. This means after data acquisition is complete, the software analyzes the sample data automatically in the background, based on the process options set in the "Analysis" and "Marker" screens (described in the Selecting analysis parameters and Selecting marker sections). The "Analysis Parameters" and "Marker" screens become enabled.
Peak Calling	Includes peak calling in the process, based on the analysis result table. This means that after analysis, peak calling will be automatically performed, based on the process options set in the "Peak Calling" screen (described in the Selecting peak calling instructions section). **Note**: This step is disabled if "Analysis" is not within the process scope.
Report	Includes report and/or export as the last step in the process. This means that the software automatically generates report and export.

3. **Optional:** Change the directory where the experiment will be saved.

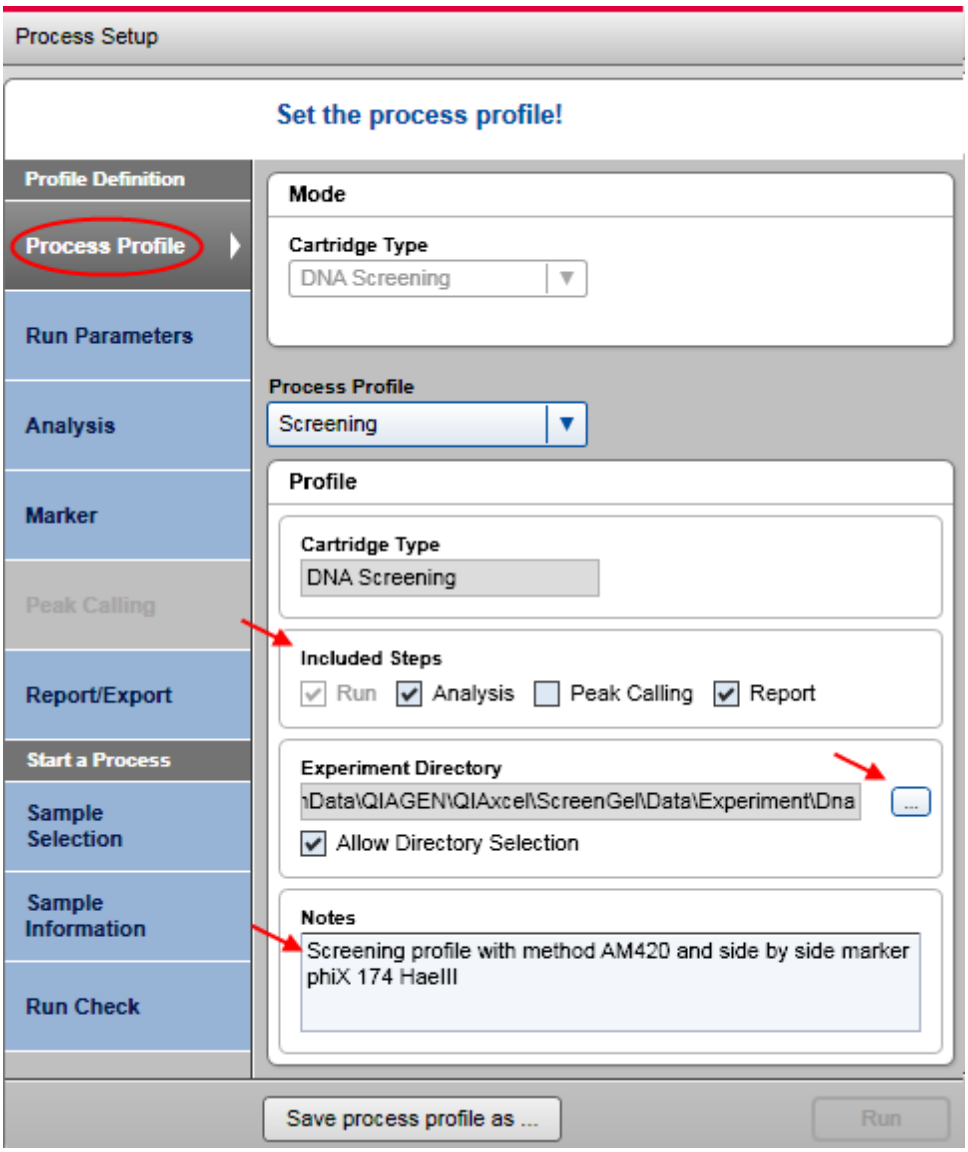
   Note: This can be a directory on the network. However, during the process, the experiment will always be saved to a local directory first (refer to Settings), and then copied to the experiment directory defined here, when the process finished.

4. **Optional:** Allow directory selection.

   Select the option to allow directory selection in the "Sample Selection" screen while preparing a process. Using this option, the run can be customized even by a user with the assigned user role "Routine User".

5. **Optional**: Edit a note in the process profile.

   Use this note field to add a short description about the intended use of the profile. This note is displayed each time the process profile is selected.



6.3.3.2 Selecting run parameters

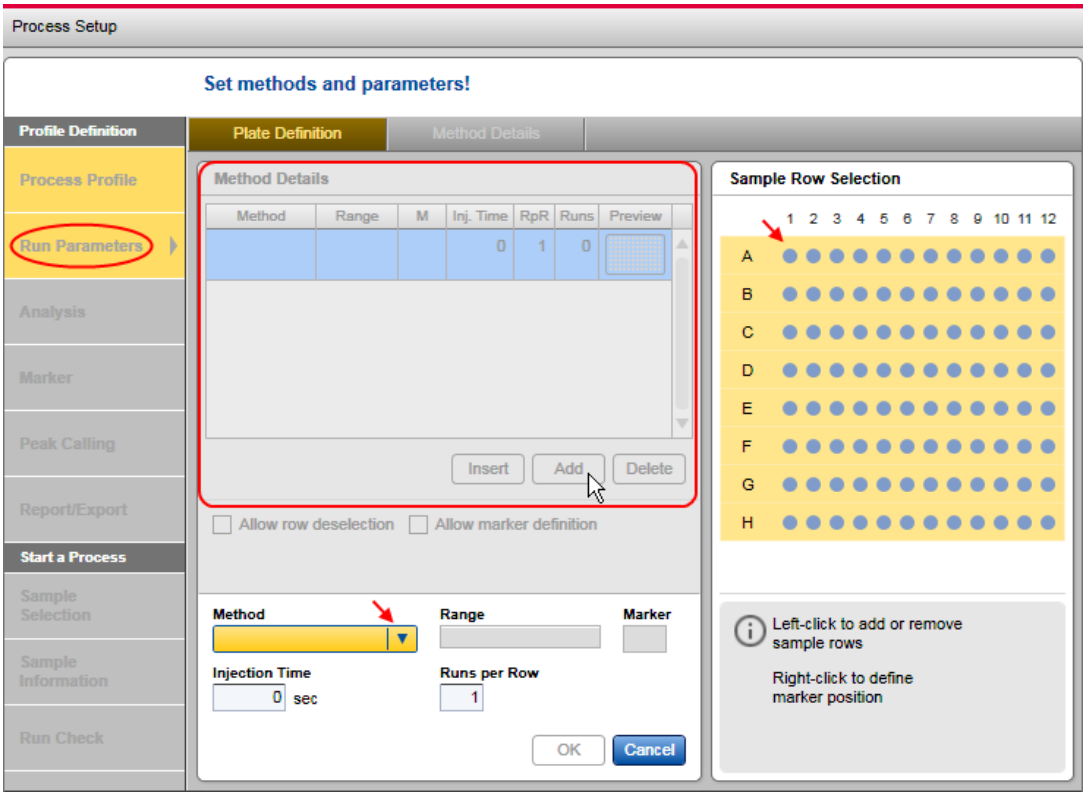
Define the methods and the rows that have to be processed with the methods. Select at least one method. In addition, the position of the size marker can also be specified.

Note: During processing, the list will be processed consecutively. For information about the correlation between run parameters and result structure, refer to the Run parameters and result structure section.

Proceed as follows:

1a. If the "Method Details" list is empty, click the "Add" button to start the first definition. A new empty entry appears in the "Method Details" list. Proceed with step 2 to specify the entry.

Note: This option is only available for users with the assigned user role "Advanced User".



Empty "Method Details" list after the "Add" button has been clicked.

1b. If the "Method Details" list is not empty you have the following options:

Add	Click the "Add" button to add a new entry at the bottom of the list. Proceed with step 2 to specify the entry. **Note**: This option is available for users with the assigned user role "Advanced User" only.
Insert	Select an entry by left-clicking and then click the "Insert" button to insert a new entry before the selected one. Proceed to step 2 to specify the entry. **Note**: This option is available for users with the assigned user role "Advanced User" only.
Modify	Select the entry you want to modify. Proceed to step 2 to modify the entry.
Delete	Select the entry you want to delete, then click the "Delete" button. The entry will be deleted from the list. Proceed to step 6. **Note**: This option is only available for users with assigned user role "Advanced User".

2. Select the rows to be processed.

   In the "Sample Row Selection" view to the right, left-click this view to add or remove a sample row to the plate. The "Range" field shows the row selection you have made.

Optional: Define the number of runs per row in the editable field "Runs per row". The method will be applied as often as you specify here.

3. **Optional**: Define the size marker position.

   Note: This position will be used for automatic analysis if the size marker is to be run side by side with the samples.

   Right-click to define the position that will contain the size marker. The "Marker" field shows the position of the marker you set.

   Note: Only one size marker position can be defined for an entry in the "Method Details" list. If you want to specify the process profile for a plate run containing a size marker at each row, create an entry for each row separately in the "Method Details" list.

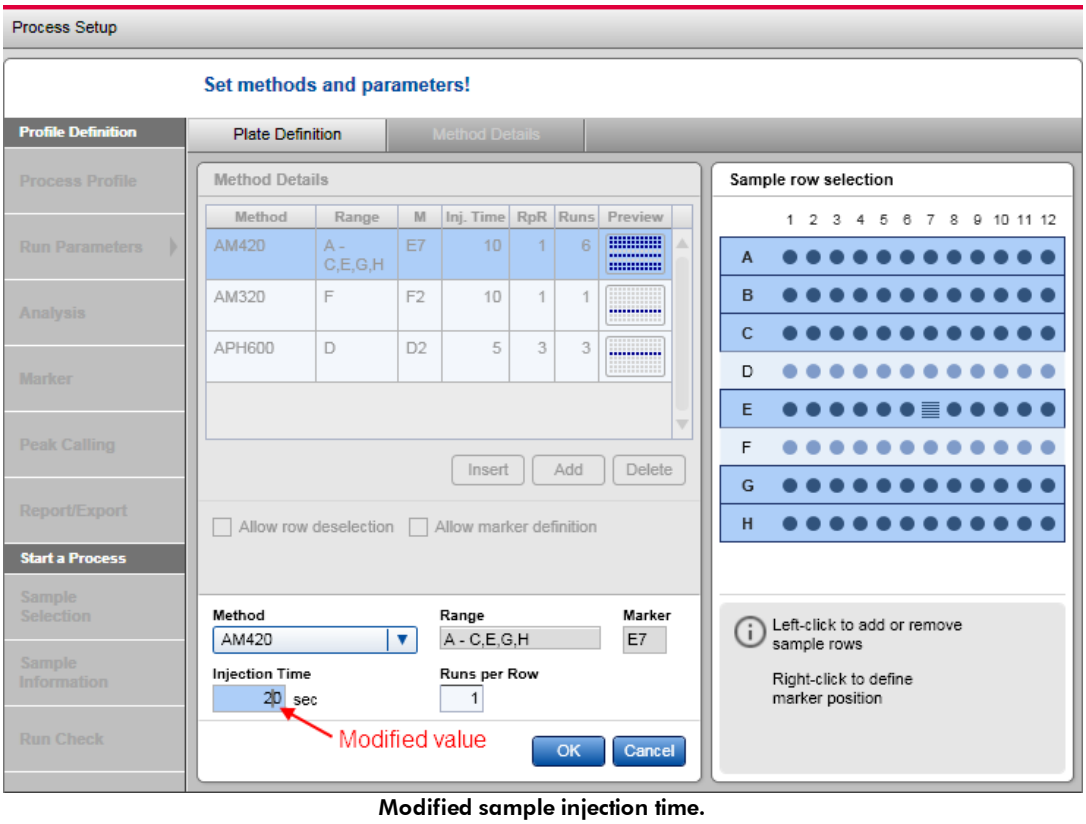
4. Select the appropriate method from the "Method" drop-down list.

   Note: This option is only available for users with the assigned user role "Advanced User".

   Note: The "Method" drop-down list only contains methods that are allowed for the cartridge type that the process profile is defined for.

   Note: A number of default methods are available for each QIAxcel Kit. For a complete list, please refer to Appendix B. Refer to the Viewing method details section if you want to look at the details of the method you have selected.

   If required, change the sample injection time in the "Injection Time" editable field. This time will be applied instead of the sample injection time defined in the method.



Modified sample injection time.

5. Click "OK" to confirm.

   Note: The "OK" button becomes enabled as soon as the rows are defined and a method is selected.

   The specified parameters appear in the entry created entry in the "Method Details" list.

   Note: Click "Cancel" to discard all specifications made during steps 2 to 5. The entry will not be created/the selected entry will not be modified.

   Note: The column "Runs" in the "Method Details" list contains the total number of runs specified by this entry: if "Range" is "A-C" and "RpR" ("Runs per Row") is "2", "Runs" will therefore be 3*2=6.

6. Define all entries in the "Method Details" list repeating steps 1 to 5.
7. **Optional**: Allow row deselection.

   Select the option to allow row deselection in the "Sample Selection" screen while preparing a process. Using this option, the run can be customized even by a user with assigned user role "Routine User".

   Note: This option is only available for users with the assigned user role "Advanced User".

8. **Optional**: Allow marker definition.

   Select the option, to allow the size marker position to be redefined in the "Sample Selection" screen while preparing a process. Using this option, the run can be customized even by a user with assigned user role "Routine User".

   Note: This option is only available for users with the assigned user role "Advanced User".

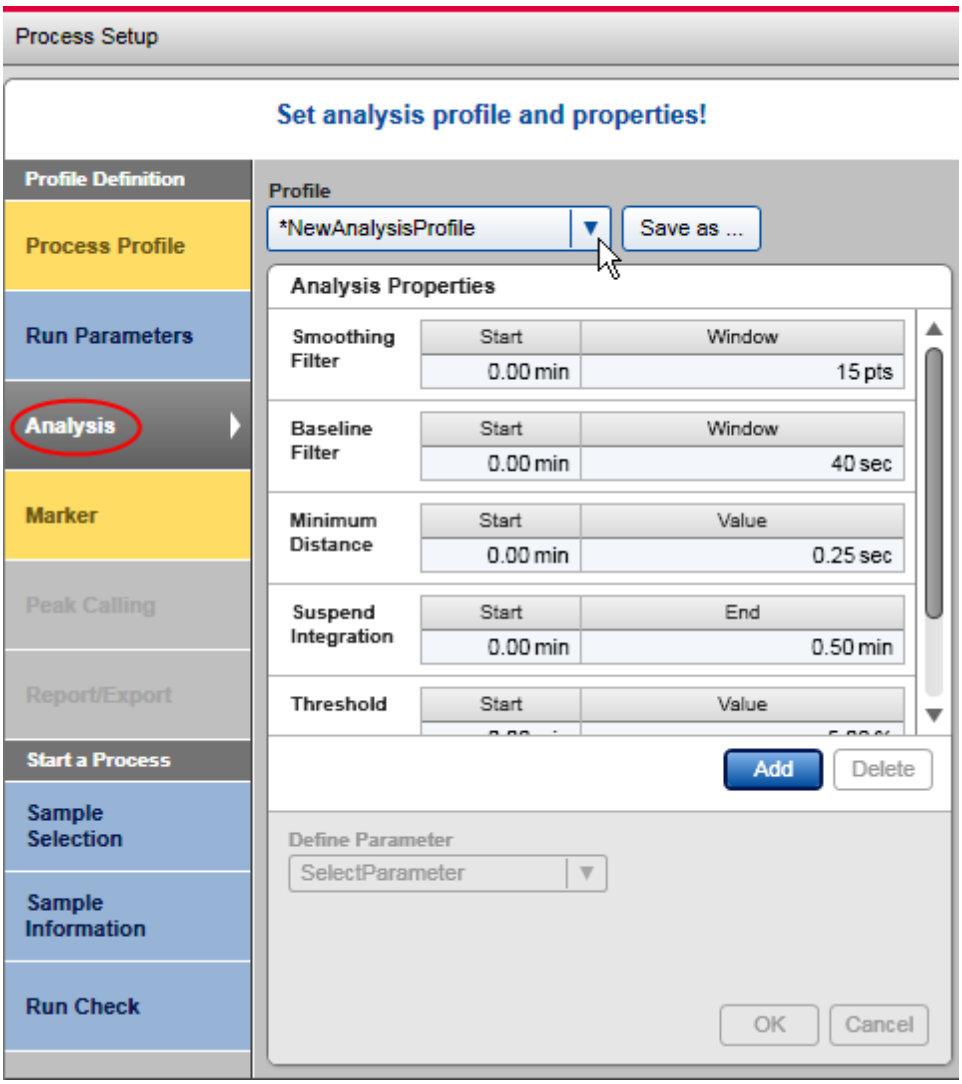
6.3.3.3 Selecting analysis parameters

Note: The "Analysis" screen is enabled only if analysis is within the scope of the process profile. For details, refer to the Selecting general process options section.

Specify the analysis parameters as follows:

1. Select an analysis profile.

   Use the "Profile" drop-down list to select the analysis profile. The analysis parameters of the selected profile are shown below the drop-down list.



Selecting an analysis profile to modify.

Note: The analysis profile will be used for fully automatic analysis of all samples.

Note: Select "NewAnalysisProfile" to define the analysis parameters from scratch. This is only possible for users with the assigned user role "Advanced User".

Note: All analysis parameters currently set in the selected analysis profile will be copied to the process profile. Further modifications of the underlying analysis profile do not affect the analysis parameters in this process profile. This prevents the process profile from unwanted changes and ensures process stability. If modifications in the underlying analysis profile are to be included in this process profile as well, include the modified analysis profile again by selecting it from the "Profile" drop-down list.

2. **Optional**: Modify the analysis parameters. You can modify the analysis parameters according to your needs in this screen as described in the Modifying an analysis profile section.

   Note: This is only possible for users with the assigned user role "Advanced User".

   Note: The modifications will only be included in this process profile. If the modified parameters are also to be included in the selected analysis profile, save the analysis profile as described below.

3. **Optional**: Save the modified analysis parameters.

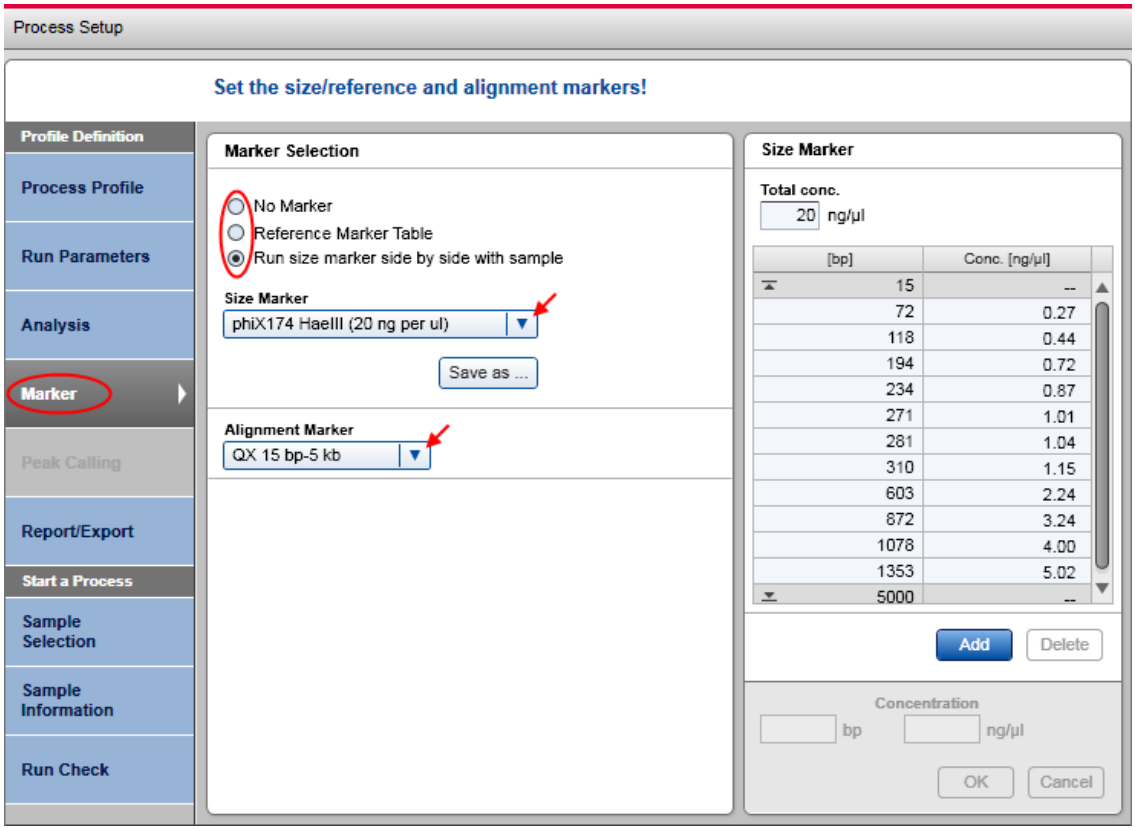
   Note: This is only possible for users with the assigned user role "Advanced User".

   The modified analysis parameters can be saved by clicking the "Save as ..." button. A dialog box appears, which includes the name of the selected analysis profile. You have two options:

   Click "OK" if you want the modifications to be saved in the selected analysis profile; enter a new unique analysis profile name to save the modified analysis parameters as a new analysis profile, then click "OK". The name of this new analysis profile and all of its analysis parameters will be included in the process profile.

6.3.3.4 Selecting marker

Note: The "Marker" screen is only enabled if analysis is within the scope of the process profile. For details refer to the Selecting general process options section.



Marker selection.

Define the markers to be used when running this process profile.

1. Select one of the size marker options.
2. Select the correct marker for the selected option.

For information about marker options see the descriptions below.

No Marker	Select this option if automatic analysis is for peak detection only. **Note**: No size marker will be used during automatic analysis, therefore determination of size and concentration is not possible.
Reference Marker Table	If analysis of size and/or determination of concentration is to be performed, select this option. The determination of size and/or concentration is based on a previously saved reference marker table. Select the reference marker table to be used from the "Reference Marker Table" drop-down list. **Note**: To ensure compatibility, the drop-down list contains only reference marker tables whose size markers were processed with the same method as defined in this process profile. The drop-down list is marked as invalid and empty if there is no compatible reference marker table. In this case, run a process with size marker side by side with the samples or create a reference marker table from a previous process (refer to the Creating a reference marker section). **Note**: If no cartridge is currently inserted, the system cannot check the compatibility of the selected reference marker table. The drop-down list is marked as invalid and empty, or it contains a previously selected reference marker table only. Insert the cartridge to be processed by the profile and select a reference marker table compatible for this cartridge and method defined in this process profile. **Note**: See the table below for explanation of the symbol at the right of the "Reference Marker Table" drop-down box:

●	The selected reference marker table is **fully compatible**. This means that the size marker used for the reference marker table was processed no more than 90 days (DNA)/60 days (RNA, protein) before with the cartridge that is currently inserted and with the same method as defined in this process profile.
●	The size marker used for the reference marker table was processed more than 90 days (DNA)/60 days (RNA, protein) before with the cartridge that is currently inserted and with the same method as defined in this process profile.
●	The size marker used for the reference marker table was processed with the same method as defined in this process profile, but with **a cartridge other than that** currently inserted.
●	The reference marker table is **not compatible with the method** defined in this process profile. This can happen if the method was changed in the "Run Parameters" screen and the reference marker table was not yet changed correspondingly. Select another reference marker table from the drop-down list that is compatible with the newly selected method.

Run size marker side by side with sample	Select this option if the plate requires a size marker. Select the size marker to be used from the "Size Marker" drop-down list. **Optional**: Change the total concentration of the size marker above the "Size Marker" table to the right, if needed. The individual concentrations of the fragments are then recalculated automatically. **Note**: This is only possible for users with the assigned user role "Advanced User". In the "Alignment Marker" drop-down list, select the alignment marker to be used in the MARKER1 position in the buffer tray. **Note**: If the "Run size marker side by side with sample" option is selected, but size marker and/or alignment marker is not specified, the "Marker" screen would be considered as invalid. **Note**: For DNA mode only: Using the correct size marker will increase the accuracy of size and concentration determination. Select the marker containing DNA fragments close to the size of your targeted DNA fragments. The DNA fragments to be analyzed must fall within the smallest and largest fragment size of the size marker. **Note**: For DNA mode only: In addition, the range of the alignment marker must cover the range of the size marker. If not, the "Size Marker" table to the right shows this discrepancy with rows highlighted in yellow and the "Marker" screen would be considered as invalid. **Note**: Refer to the Selecting run parameters section for information about how to define the position of the size marker.

6.3.3.5 Selecting peak calling instructions

Note: The "Peak Calling" screen is enabled only if analysis and peak calling are within the scope of the process profile. For details refer to the Selecting general process options section.

Refer to the Peak Calling section for an explanation of the peak calling concept.

Define the instruction for peak calling.

1. Select a peak calling instruction.

   Use the "Peak Calling Instruction" drop-down list to select a predefined peak calling instruction. The instruction definition is shown below the drop-down list.

   Note: All parameters currently set in the selected peak calling instruction will be copied to the process profile. Further modifications of the underlying peak calling instruction do not affect the peak calling parameters in this process profile. This protects the process profile from unwanted changes and ensures process stability. If modifications in the underlying peak calling instruction are also to be included in this process profile, include the modified peak calling instruction again by selecting it from the "Peak Calling Instruction" drop-down list.

   Note: Select "NewPeakCallingInstruction" to create a new instruction (for "Advanced Users" only). The "Peak Calling" screen is highlighted in yellow because the new peak calling instruction is still empty. Proceed to step 2 to define the instruction.

2. Modify the peak calling instruction. The peak calling instruction can be modified as required in this screen as described in the Modifying a peak calling instruction section.

   Note: This can only be carried out by users with the assigned user role "Advanced User".

Note: The modifications will only be included in this process profile. If the modifications are also to be included in the selected peak calling instruction, save the peak calling instruction as described below.

3. Save the modified peak calling instruction.

   Note: This can only be carried out by users with the assigned user role "Advanced User".

   The modified peak calling instruction can be stored by clicking the "Save as ..." button. A dialog box appears containing the name of the selected peak calling instruction. You have two options: Click "OK" if the modifications are to be stored in the selected peak calling instruction; enter a new unique peak calling instruction name to save the modifications to a new peak calling instruction, then click "OK". The name of this new peak calling instruction and all of its parameters will be included to the process profile.

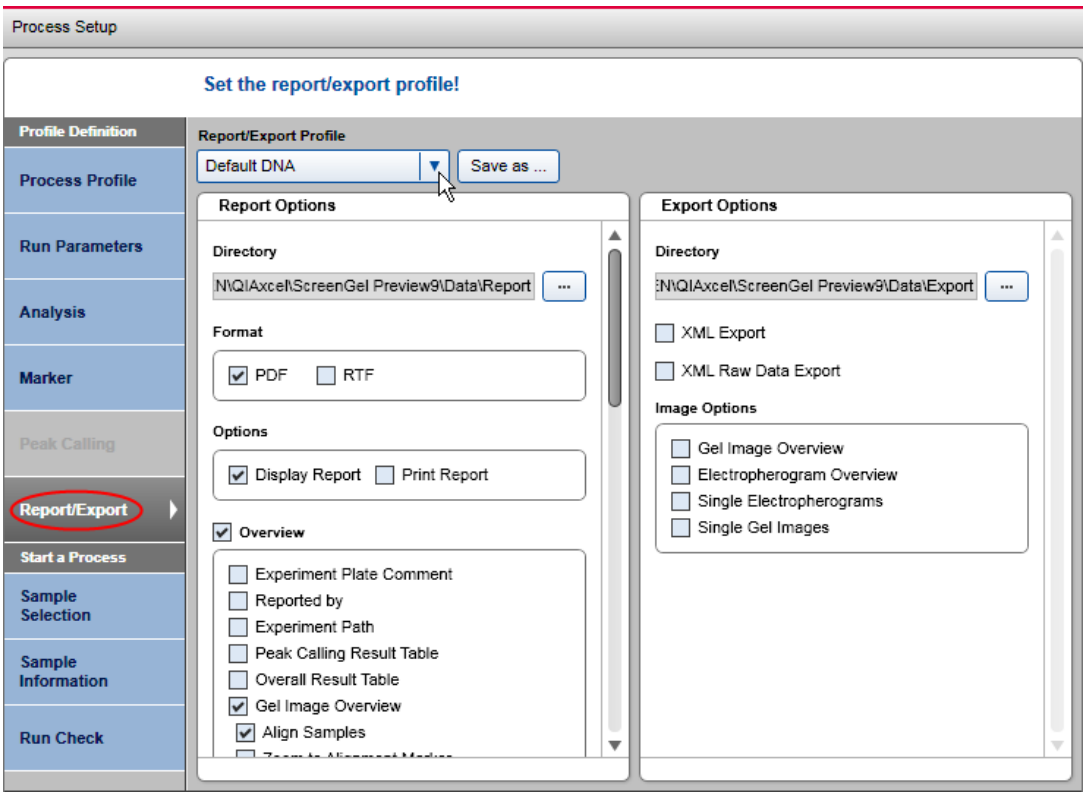
6.3.3.6 Selecting report/export parameters

Note: The "Report/Export" screen is enabled only if "Report" is within the scope of the process profile. For details, refer to the Selecting general process options section.

Specify the report and export parameters as follows:

1. Select a report/export profile.

   Use the "Report/Export Profile" drop-down list to select the report/export profile. The parameters of the selected profile are shown below the drop-down list.



Selecting a report/export profile.

Note: All report/export parameters currently set in the selected report/export profile will be copied to the process profile. Further modifications of the underlying report/export profile do not affect the report/export parameters in this process profile. This prevents the process profile from unwanted changes and ensures process stability. If modifications in the underlying report/export profile are also to be included in this process profile, include the modified report/export profile by selecting it from the "Report/Export Profile" drop-down list.

Note: Report/export profiles with the option "Use Images as Displayed" selected are not listed in the "Report/Export Profile" drop-down list. This option is available in the analysis environment only. Refer to the Report/Export options section for more information.

2. Modify the report/export parameters.

   The report/export parameters can be modified as required in this screen. Refer to the Report/Export options section for more information.

   Note: The modifications will only be included in this process profile. If the modified parameters are also to be included in the selected report/export profile, save the report/export profile as described below.

   Note: A report/export profile is only applicable if at least one format check box ("PDF" or "RTF") and one of the content options ("Overview" or "Sample Details") is selected for report, or if one check box is selected for export. The check boxes and the "Report/Export" screen are highlighted in yellow if no selection is made.

3. Save the modified report/export parameters.

   Note: This can only be carried out by users with the assigned user role "Advanced User".

   The modified report/export parameters can be saved by clicking the "Save as ..." button. A dialog box appears, which includes the name of the selected report/export profile. You have two options: Click "OK" if the modifications are to be stored in the selected report/export profile; enter a new unique report/export profile name to save the modified report/export parameters to a new report/export profile, then click "OK". The name of this new report/export profile and all of its parameters will be included in the process profile.

6.3.3.7 Run parameters and result structure

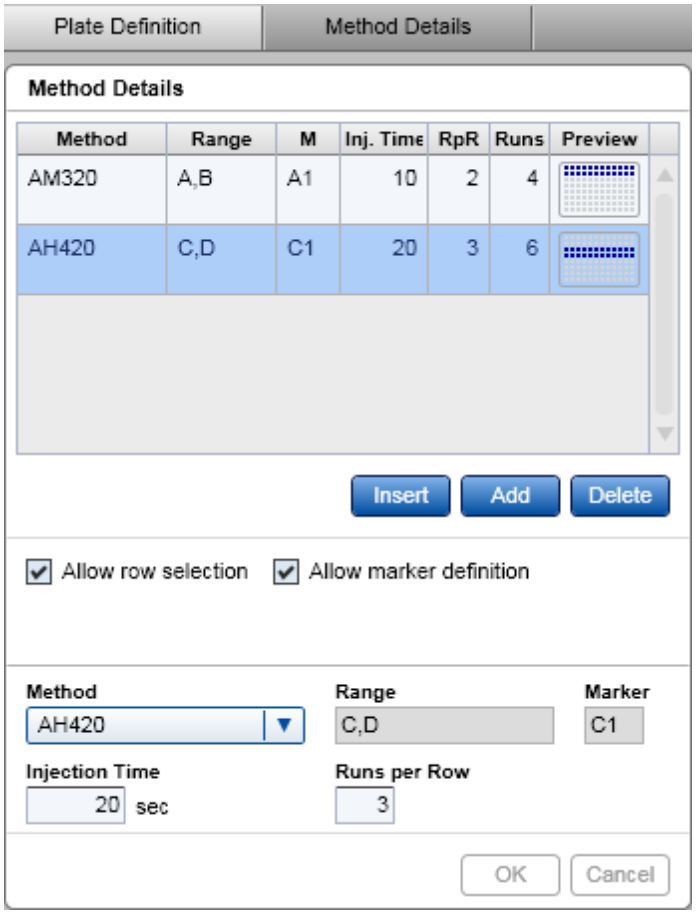
This section provides an example so that the relation between process definition and the structure of the result can be described:

With a QIAxcel DNA Screening Cartridge:

- Rows A and B will be run twice with method AM320, with size marker at position A1
- Rows C and D will be run 3 times with Method AH420, with the same size marker at position C1

The same alignment marker will be used for both methods.

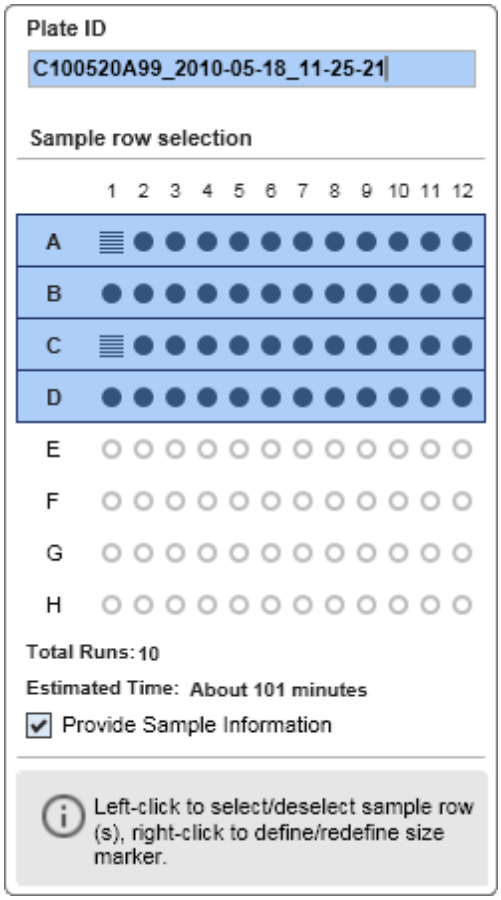
See the "Run Parameters" and "Sample Selection" screens of the process definition:



"Run Parameters" screen.

Two entries were defined because of the different methods. The rows and size marker positions were defined for each method, as well as for the runs per row (column "RpR" in the "Method Details" list). In the "Runs" column the total number of runs for each method is listed.

During the process, the software first runs method AM320 in the order row A and B (first run), and row A and B (second run). It then runs method AH420 in the order row C and D (first run), row C and D (second run), and row C and D (third run).



"Sample Selection" screen.

The "Plate ID" will be used as the name of the results.

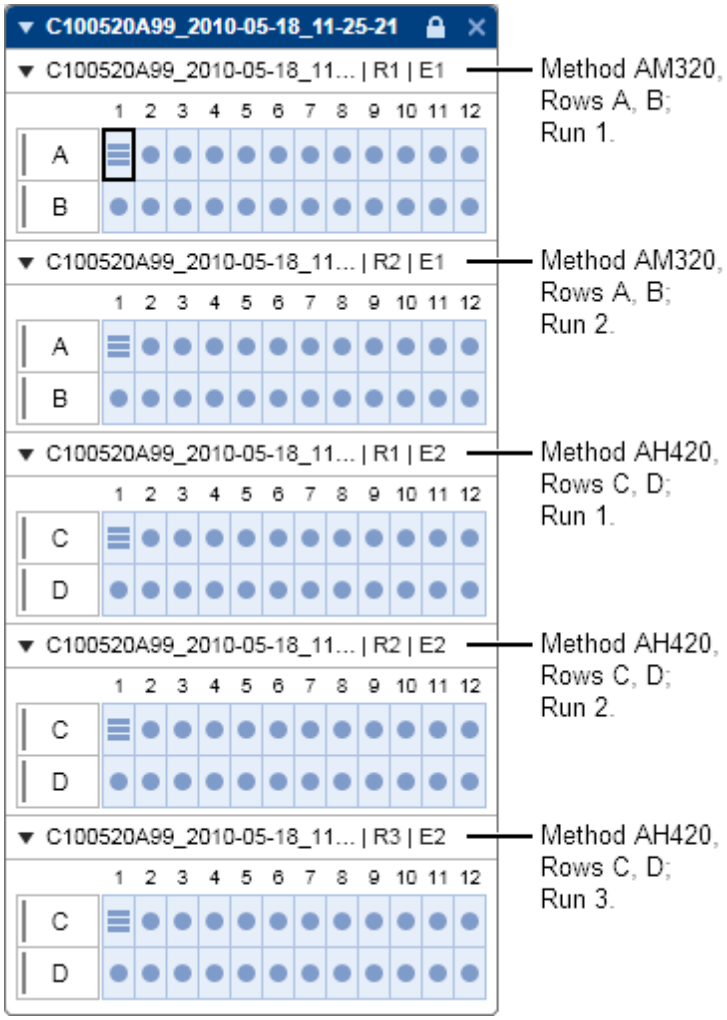
The Sample row selection shows a summary of the run definition in the "Run Parameters" screen.

The total number of runs ("Total Runs") in this example is 10:

2 times A and B = 4 runs for method AM320

3 times C and D = 6 runs for method AH42

When the process is finished, the sample data are presented in the "Analysis" environment in the "Experiment Explorer":



Experiment generated by the process.

All sample data generated by the process are combined into one experiment and named according to the "Plate ID", which was specified in the "Sample Selection" screen.

All sample data are grouped by so called "plates" as they were generated by the process.

The name of the plate identifies the run. It is combined with:

Experiment name	The experiment name is created from the "Plate ID" specified in the "Sample Selection" screen.
R#	Run number, where "#" represents a number, starting from 1. In this example for method AM320, the run numbers R1 and R2 are generated.
E#	Entry number (entry in the "Method Details" list of the "Run Parameters" screen), where "#" represents a number starting from 1. In this example, the entry numbers E1 and E2 are generated, because the "Method Details" list contained 2 entries.

Therefore, the sample data for method AM320 for rows A and B are listed first and also separately for each run.

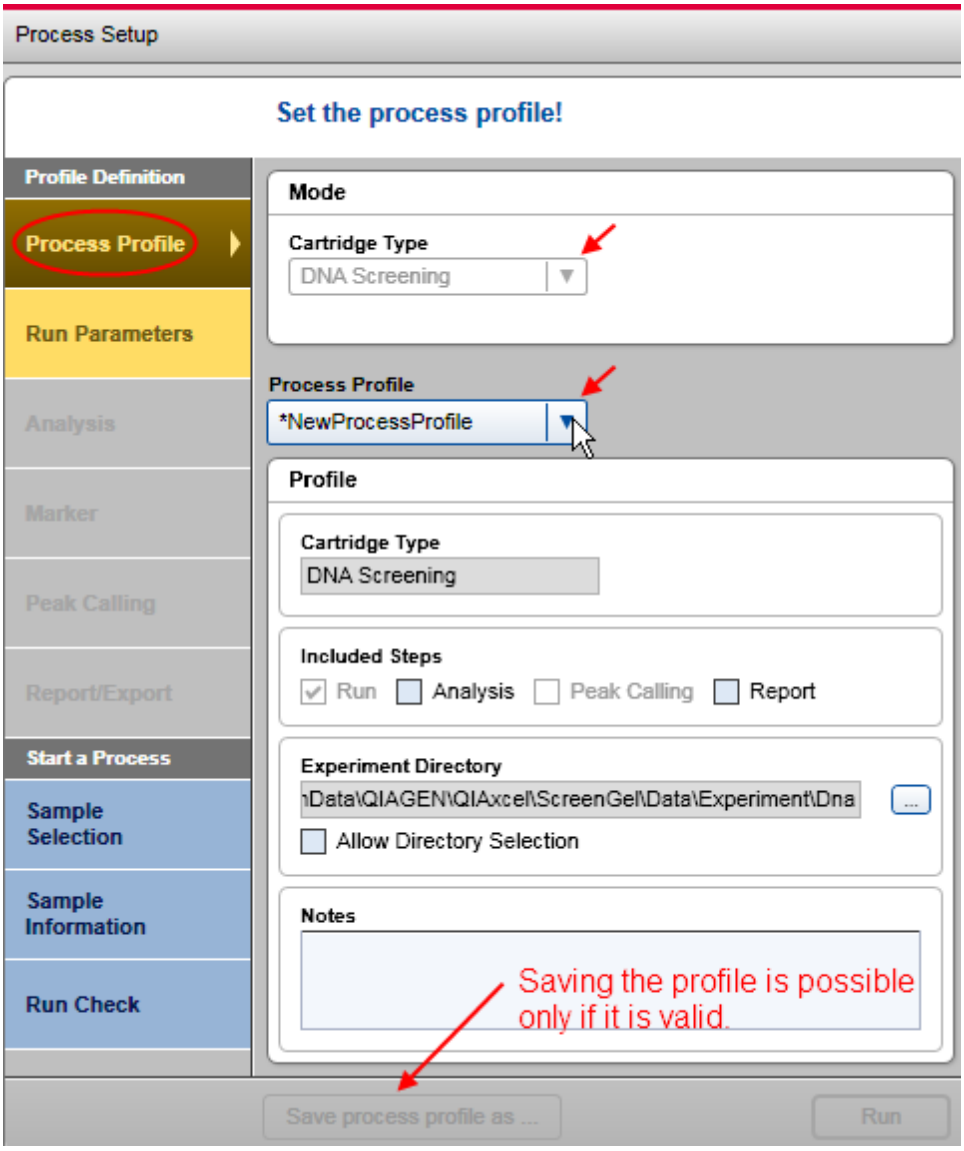
6.3.4 Creating a new process profile

Note: Only users with the assigned role "Advanced User" can create a new process profile.

To create a new process profile, proceed as follows:

1. Open the "Process" environment.

   If not open, switch to the "Process" environment by clicking the "Process" environment icon. Select the "Process Profile" screen.



Main steps for creation of a new process profile.

Note: If the last process only just finished, click the "Back to Wizard" button at the bottom right.

2. Select cartridge type.

   Select the cartridge type that is to be used for the new process profile.

Note: Each process profile is related to a certain cartridge type. Therefore, the system can ensure that a process (i.e., data acquisition) can be started only if a cartridge with correct cartridge type is inserted.

Note: If the instrument is connected, the system automatically detects the inserted cartridge and the cartridge type cannot be changed. If you want to create the process profile for another cartridge type, remove the cartridge, or at least the cartridge key, or disconnect from the instrument.

3. Select a process profile.

   Use the "Process Profile" drop-down list to select a process profile. The selected profile serves as a template for the creation of the new profile.

   Note: Select "NewProcessProfile" to create a process profile from scratch. The system will show "*NewProcessProfile" after selection. This can only be carried out by users with the assigned role "Advanced User".

3. Set the process profile options according to your needs.

   See section Process profile options for detailed information.

4. Save the modified process profile under a new name.

   Click the "Save Process Profile as ..." button below process setup and enter a new unique profile name in the dialog box that appears.

   Note: This can only be carried out by users with the assigned user role "Advanced User".

   Note: If there are process profile screens containing incomplete or inconsistent data highlighted in yellow, the "Save process profile as..." button is disabled. Select the marked process profile screens and correct the data. If all data are correct, the "Save process profile as..." button becomes enabled and the process profile can be saved.

6.3.5 Viewing method details

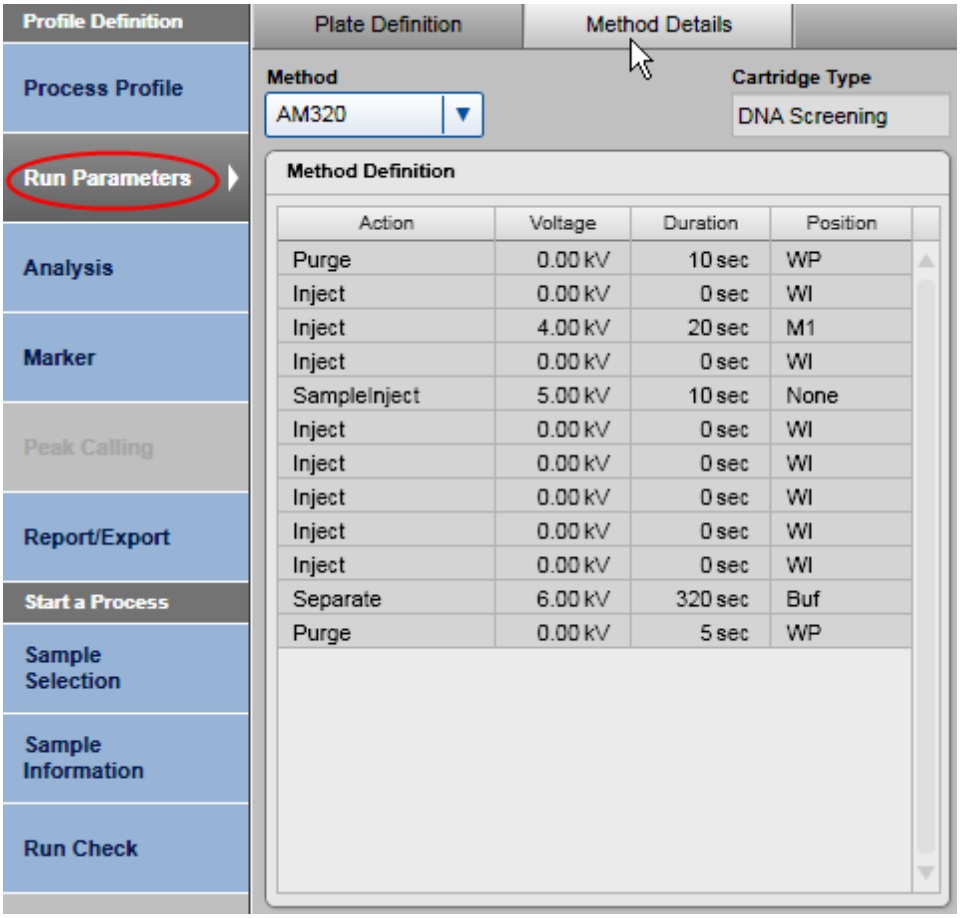
During definition of a process profile, it is possible to view the details of a method.

Note: This function is available for users with the assigned role "Advanced User" and "Basic User" only.

Proceed as follows:

1. Select a process profile in the "Process Profile" screen.
2. Switch to the "Run Parameters" screen. Select the entry containing the method you want to view in the "Plate Definition" tab .
3. Switch to the "Method Details" tab.
4. Select another method to view, if required.

   Note: Selecting another method modifies the entry in the "Plate Definition" tab you came from. Ensure you have selected the correct method you want to process.



"Method Details" screen.

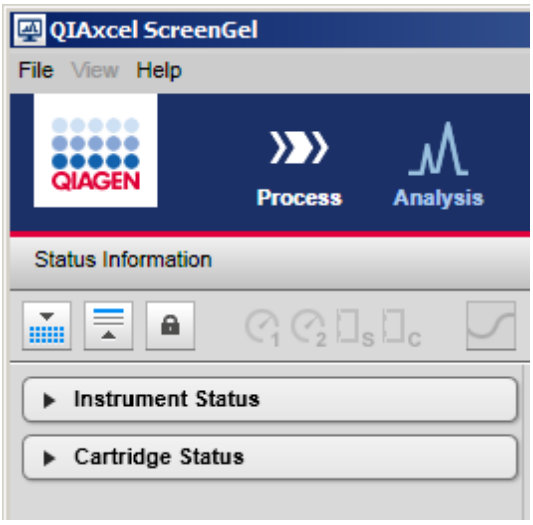
All actions defined in the method are listed. During the run the actions will be performed sequentially.

For more information about what the position abbreviations mean, see the "Instrument Status" section of the "Status Information" panel to the left of the "Process" environment.

6.3.6 "Status Information" panel

The left panel of the screen in the "Process" environment is called the "Status Information" panel. It is divided into

- A toolbar at the top
- "Instrument Status"
- "Cartridge Status"



"Status Information" panel

"Instrument Status" and "Cartridge Status" can be collapsed and expanded.

The t**oolbar** buttons and status icons are explained in the following table.

"Load Position" button. Click the button to move the buffer tray to the front of the instrument to load samples and buffer.

Note: The motors will not move if either the sample door or cartridge door is open.

"Wash Park Position" button. Click the button to move the cartridge to the "Wash park" position of the buffer tray.

Note: The motors will not move if either the sample door or cartridge door is open.

Indicates that the currently inserted QIAxcel gel cartridge is "**latched**". Click the button to unlatch the QIAxcel gel cartridge.

Important: If the "Pressure 1" status is low, increase system pressure before unlatching. Releasing the cartridge latching with reduced pressure may damage the instrument!

Indicates that the currently inserted QIAxcel gel cartridge is "**unlatched**". Click the button to latch the QIAxcel gel cartridge.

Important: If the "Pressure 1" status is low, increase system pressure before unlatching. Releasing the cartridge latching with reduced pressure may damage the instrument!

"Pressure 1" status: OK/Low. OK indicates adequate pressure for the sample run. LOW indicates that the N_2 pressure is sufficient for the current sample run; however, the N_2 cylinder should be replaced once the run of the current sample row has finished.

"Pressure 2" status: OK/Low. OK indicates adequate pressure for the sample run. LOW indicates that the N2 pressure is insufficient for the current sample run and the analysis will not be performed. The N_2 cylinder should be replaced.

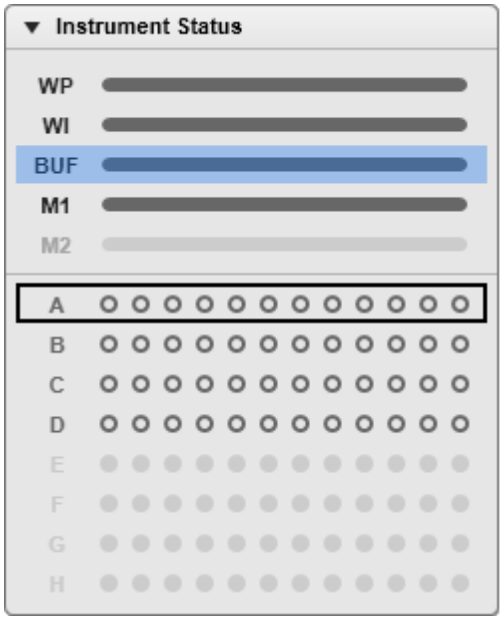
Sample door: Closed/Open.

Cartridge door: Closed/Open.

Connection status: Connected, disconnected, and connection is being established with the QIAxcel Advanced instrument.

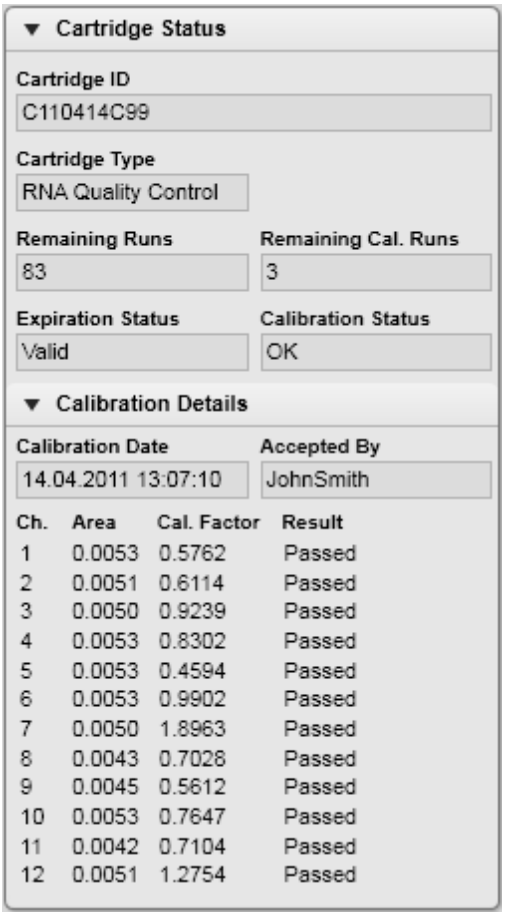
Note: If disconnected, the icon can be clicked to connect to the instrument.

The "Instrument Status" panel displays the buffer tray and sample plate. The current position of the capillaries of the QIAxcel gel cartridge is highlighted when the process is running. In the example below, the sample rows A-D are processed with the same method.



"Instrument Status" panel.

The "Cartridge Status" panel displays information about the QIAxcel gel cartridge currently inserted, such as cartridge ID, cartridge type, remaining number of runs, remaining number of calibration runs, expiration status, and calibration status. When opening the "Calibration Details" expander, additional calibration details are shown.



"Cartridge Status" panel.

Note: Calibration status "Not OK" means that the cartridge is not calibrated and needs calibration. For information about calibration, refer to the Calibrating a cartridge section.

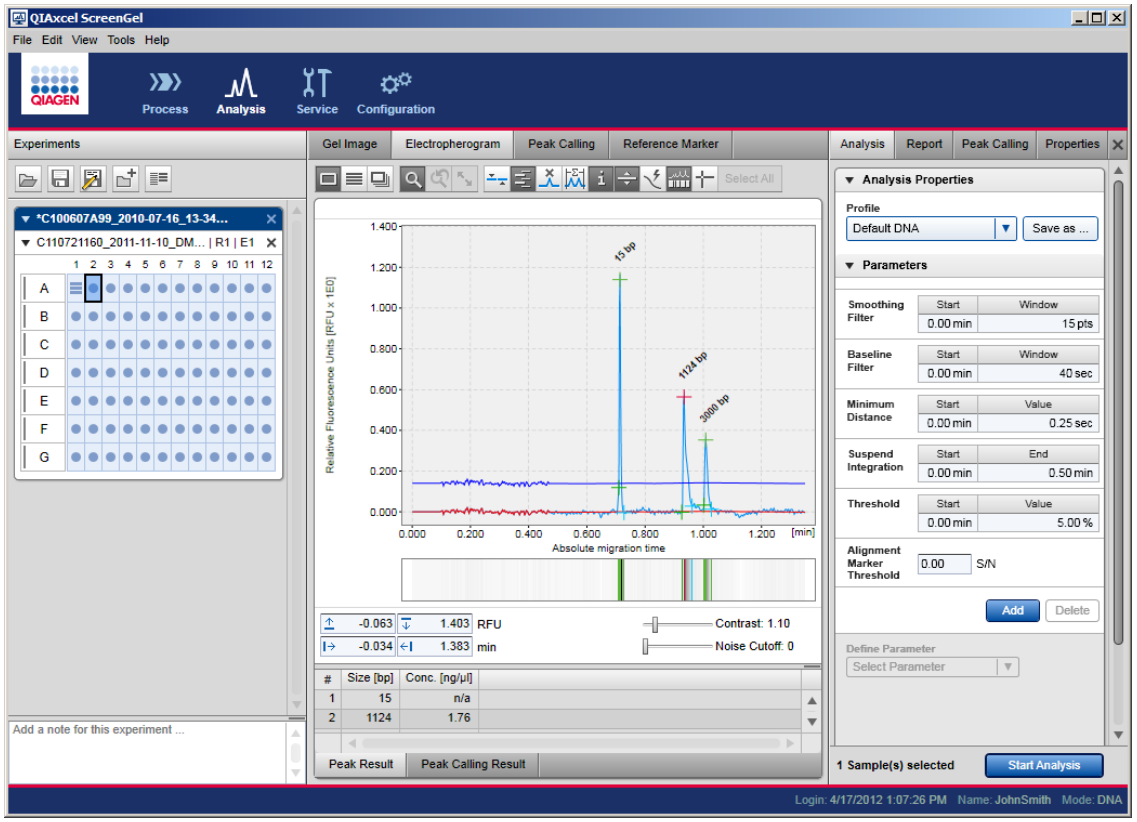
Note: The "Status Information" panel is shown in the "Process" environment and the "Service" environment.

6.4 Analysis

The "Analysis" environment provides sophisticated visualizations and analysis algorithms for electropherograms acquired by the QIAxcel Advanced instrument.

The software provides several customizable views for sample raw data, for example, a gel view, a single electropherogram view, and electropherogram superposition view. Electropherogram views also visualize analysis results, enabling fast assessment of the results.

The analysis algorithms provided by the QIAxcel ScreenGel software automatically determine a variety of peak properties. Analysis algorithms can be applied to single samples or collections of samples (called experiments), and can be customized by the user. The size and concentration of analytes can be determined. In addition, in the RNA mode, the 28S/18S ratio and concentration of total RNA can be established, and in the protein mode, the relative abundance of proteins can be determined. After the automated analysis, the analysis results can be adjusted.



"Analysis" environment with active "Electropherogram" screen, "Experiment Explorer" to the left, and "Analysis" panel to the right.

6.4.1 Handling samples and experiments

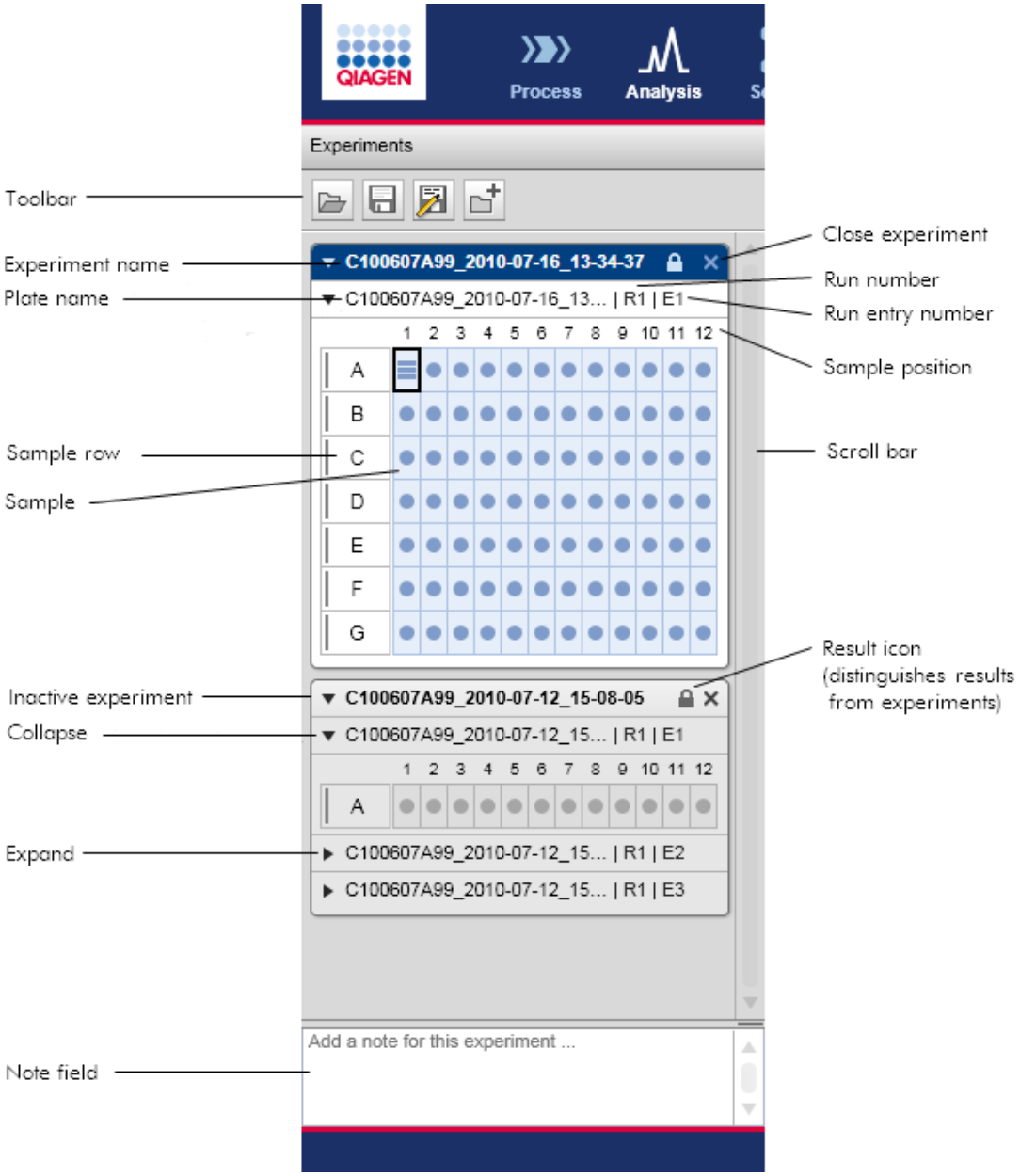
The "Experiment Explorer" in the "Analysis" environment displays samples in a concise manner and provides functionality to load and manage samples.

After a process is completed, the result data are saved in an experiment. If the "Analysis" environment is selected, the experiment is automatically loaded in the experiment explorer.

An experiment groups samples by plates and rows in the order that they were processed. For detailed information, refer to the Run parameters and result structure section.

Several experiments can be loaded, but only one experiment can be active at a time. The samples in the experiment can be visualized and analyzed. A note for the active experiment can be entered in the note field at the bottom of the explorer.

Customized experiments can be created to combine sample result data from different experiments. Refer to the Customizing experiments section for detailed information.



"Experiment Explorer".

The experiment explorer toolbar has the following buttons:

Load experiment from disk: Refer to the Loading sample data section for detailed information.

Save: Save the active experiment to disk. Refer to the Saving an experiment section for detailed information.

Move/rename: Save the active experiment; allows the name and directory to be changed. Refer to the Saving an experiment section for detailed information.

Note: This function does not create a copy of the experiment.

Create new experiment: Refer to the Creating a new experiment section for detailed information.

6.4.1.1 Meaning of sample icons

In the "Experiment Explorer", samples are symbolized by a well and size markers by a ladder

These symbols vary slightly according to the analysis, visualization, and selection status:

Analyzed	Meaning	Not analyzed
	Not visualized, not selected.	
	Visualized, not selected.	
	Not visualized, selected.	
	Visualized, selected.	

The current focus sample has, in addition, a border . This sample is displayed in the single electropherogram view and you can inspect its properties.

The "Size Marker" property of a sample can be changed by using the sample context menu. Use the "Size Marker" option to toggle.

A reference marker can be created afterward from samples with the "Size Marker" property.

6.4.1.2 Loading sample data

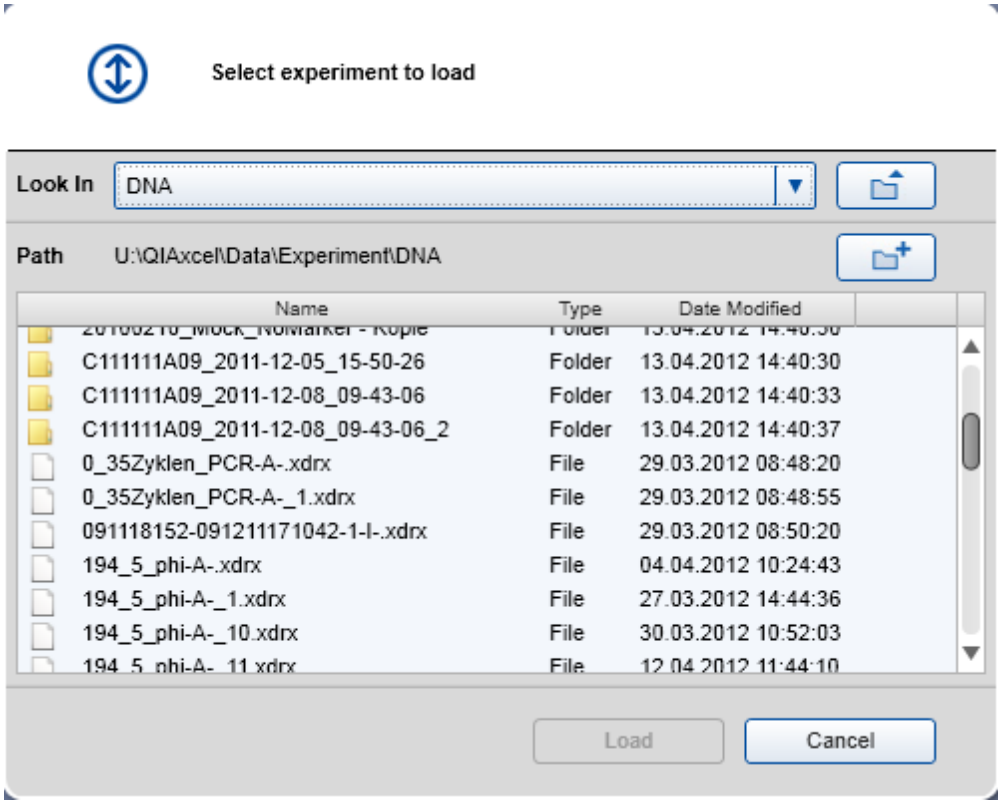
To load samples from the disk, proceed as follows:

1. Click at the top of the "Experiment Explorer".
2. A file dialog appears, showing all experiments that were created in the current run mode (e.g., in DNA mode, you will not see RNA experiments). Navigation starts in the most recently opened directory, or otherwise in the default experiment directory. You can navigate to a different directory.

   Note: To open calibration results, select the path ending with "[Calibration Results]"
3. Select the experiment from the list by double-clicking it, or clicking it with the mouse and clicking "Load file".

4. The experiment will be loaded and displayed in the "Experiment Explorer".

   Note: If there were experiments already loaded in the "Experiment Explorer", the experiment just opened will be displayed as the last experiment, at the bottom. The newly loaded experiment automatically becomes active.



The file dialog for loading an experiment.

Representation of an experiment on disk

An experiment is represented on disk as a file with the name of the experiment. The file extension depends on the mode used to create the experiment (**.xdrx** for DNA, **.xrrx** for RNA, **.xprx** for protein, and for calibration data created during cartridge calibration, **.xcdrx**, **.xcrrx**, and **.xcprx**, respectively).

Loading experiments of previous software versions

To load an experiment that was created with a previous QIAxcel ScreenGel software version, proceed as described above.

In version 1.0 of QIAxcel ScreenGel, an experiment was represented on disk as a folder with the name of the experiment.

The folder contained a file with the name of the experiment, describing the experiment structure. The extension of this file was dependent on the mode used to create the experiment (**.xdr** for DNA, **.xrr** for RNA, **.xcr** for calibration data created during cartridge calibration).

In addition, the folder contained several files, each containing the sample data of a sample row. The file names were extended based on the experiment name.

When such an experiment is loaded with QIAxcel ScreenGel software version 1.1, it is automatically converted (migrated) to the newest version. After saving the experiment, the folder with the experiment and sample files is replaced by a single experiment file with the appropriate new file extension (see above).

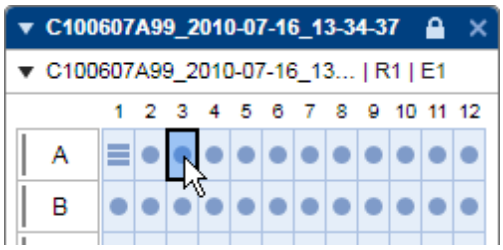
Note: A migrated experiment cannot be opened by previous software versions any more.

Note: When an RNA experiment is loaded, the search criteria for the 18S and 28S peak in the reference marker table are automatically converted to a peak calling instruction.

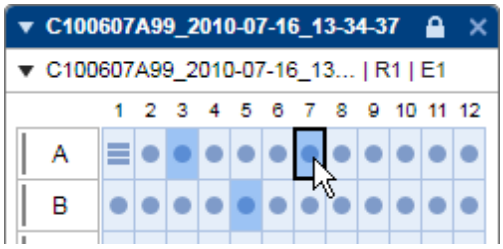
For loading experiments from the BioCalculator software, refer to the Importing BioCalculator Data section.

6.4.1.3 Selecting samples

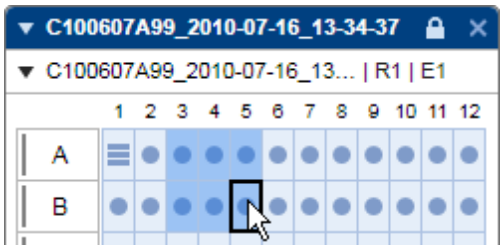
In the "Experiment Explorer" samples inside the active experiment can be selected. For more information about activating an experiment, see the Activating an experiment section.



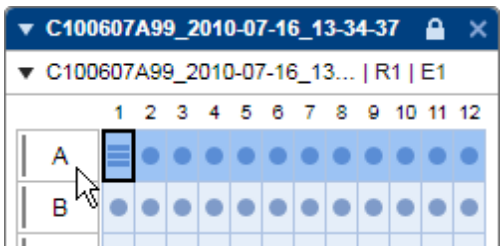
Select an individual sample with a left-click.



To select multiple single samples, simultaneously hold the "Ctrl" key and left-click the samples.

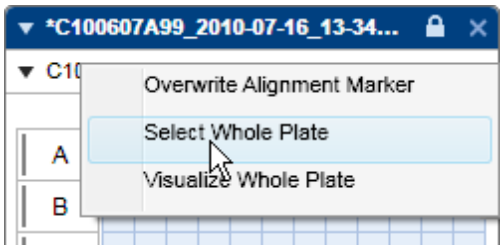


To select multiple samples in a rectangular area, simultaneously hold the "Shift" key and — for this example — left-click the samples A3 and B5.

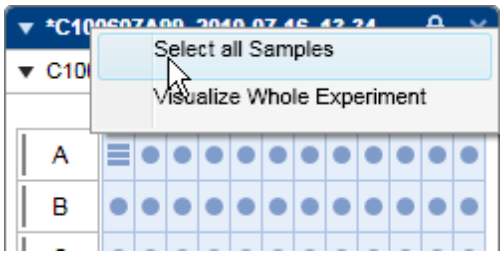


To select all samples in a row, left-click the row letter.

To select multiple rows, hold the "Ctrl" or "Shift" keys simultaneously.



To select all of the samples of a plate, right-click the plate name and select the context menu option "Select Whole Plate".



To select all of the samples of the experiment, right-click the experiment name and select the context menu option "Select all Samples".

Switch the focus by left-clicking a sample. During sample selection, the last sample selected has the focus.

If samples from different experiments need to be selected, create a new customized experiment containing these samples. For more information about customized experiments see the Customizing experiments section.

6.4.1.4 Selecting samples for analysis or report

Here the selection inside the view is relevant — not the selection in the "Experiment Explorer". The selection of samples depends on the view:

View	Single sample selection	Multiple sample selection
Gel Image	Select a single sample by clicking the gel lane header of the sample. Selection of a sample for analysis in the "Experiment Explorer" is not possible in this environment.	Selection of multiple samples can be performed by clicking the gel lane headers using the "Shift" or "Ctrl" key (just as in the Windows explorer). Alternatively, you can select all visualized gel lanes by clicking the "Select all" key in the tool bar.
Single Electropherogram	Select a single sample in the "Experiment Explorer". In this view, the visualized sample will be analyzed.	Not possible in this view.
Electropherogram Overview	Select a single sample by clicking the electropherogram of the sample. Selection of a sample for analysis in the "Experiment Explorer" is not possible in this environment.	Selection of multiple samples can be performed by clicking the electropherograms using the "Shift" or "Ctrl" key (just as in the Windows explorer). Alternatively, you can select all visualized electropherograms by clicking the "Select all" key in the tool bar.
Electropherogram Superposition	Not possible in this view.	All samples included in the diagram are selected automatically.

6.4.1.5 Expanding and collapsing

For a greater overview, you can collapse experiments or plates, regardless of whether the experiment is active or not.

To collapse an experiment:

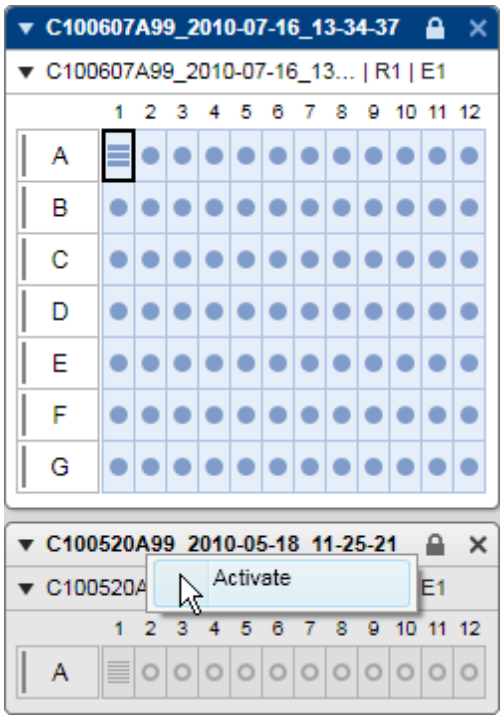
1. Click ▼ to the left of the experiment name. The entire experiment collapses down to the experiment name only.
2. Click ▶ to expand it again.

Note: You can collapse a single plate inside an experiment by clicking ▼ to the left of the plate name. The plate collapses down to the plate name only. Click ▶ to expand it again.

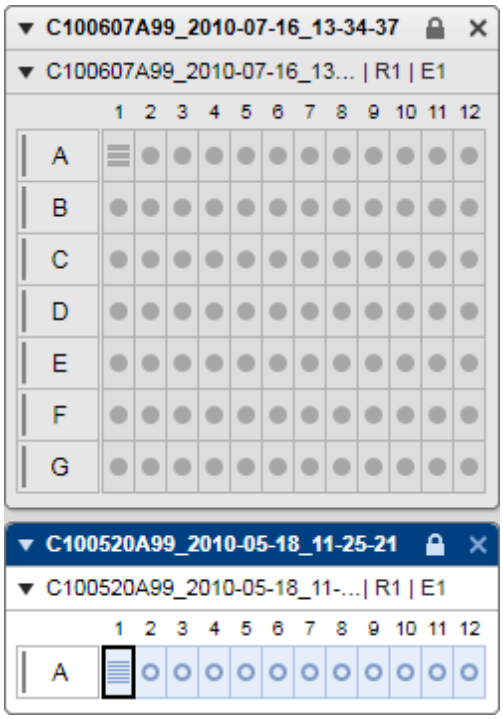
6.4.1.6 Activating an experiment

Only one experiment can be active at a time. The samples in the active experiment can be visualized and analyzed.

To activate an experiment in the "Experiment Explorer", right-click the experiment and select "Activate" from the context menu or double-click the experiment header.



Activating an experiment using the context menu.



The experiment is now active.

The previously active experiment will be deactivated automatically. If this experiment was modified, the system asks you whether the changes should be saved or not. Click "Yes" to save or "No" to discard the changes. Select "Cancel" to cancel activation. For more information about saving experiments, see the Saving an experiment section.

Note: Version 1.0 legacy experiments cannot be deactivated. Instead, they will be closed if you activate another experiment. You can avoid this by saving them in the new format.

6.4.1.7 Saving an experiment

To save the active experiment to the disk, click the "Save" button at the top of the "Experiment Explorer".

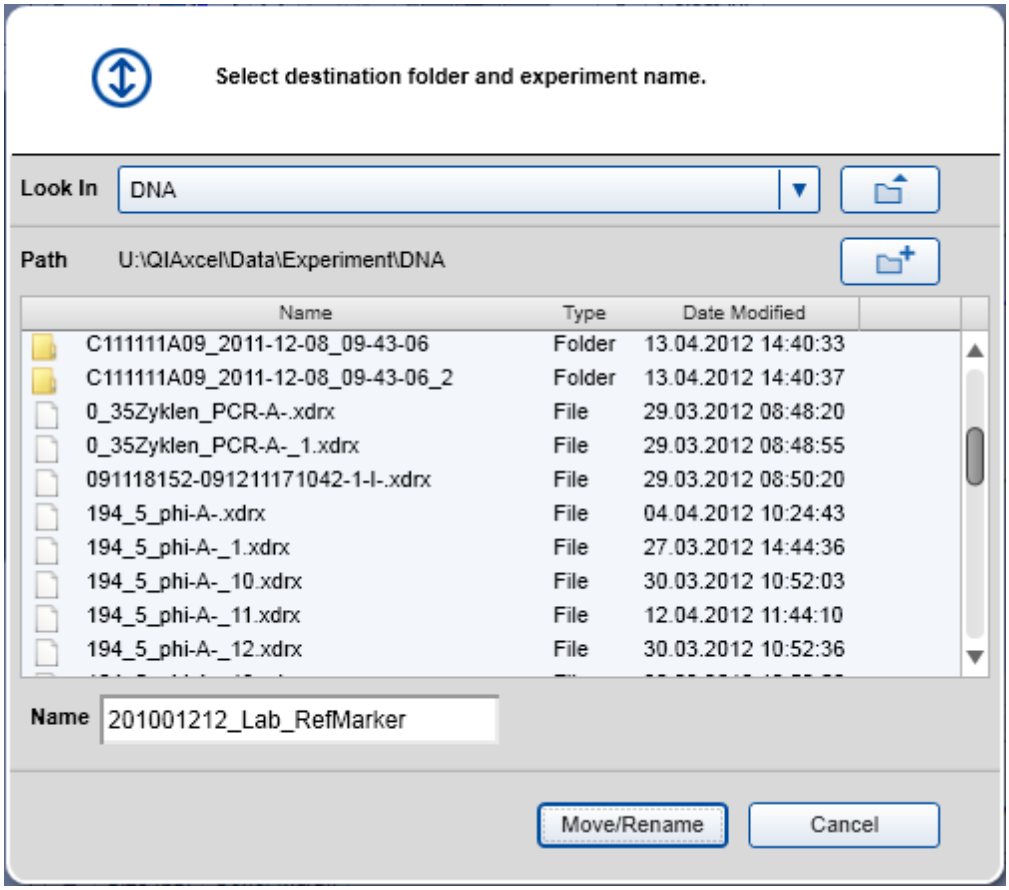
All modifications made to this experiment will be saved, as specified in the settings. This includes analysis results, as well as information about the configuration of the visualization.

Note: Sample data cannot be saved individually.

If you want to save the active experiment to another directory, use the "Move/rename" button . This will open a file dialog for choosing a different directory and experiment name.

Note: To avoid data redundancy, the previous experiment file will be removed.

The same file dialog opens if the experiment was created in the experiment explorer and has not yet been saved to disk.



The file dialog for saving an experiment.

The file dialog enables navigation to the directories of the disk, creation of a new directory, and allows the user to choose the new name of the experiment. The appropriate file extension will be appended automatically.

Note: The experiment name is restricted to 40 characters.

Information stored in the experiment

The following information is stored in the experiment:

- Experiment structure.
- Visualization information: visualization status of the samples (not for superimposition), sample order in the visualization.

The following information is saved in each sample since it can differ from sample to sample:

- Run information: all run parameters, including cartridge information, parameters of the method used, sample injection time, and separation time. The run information is stored immediately after the process has finished and will not be changed later.
- Analysis information, if the sample has been analyzed: includes analysis parameters, reference marker table used during analysis, and peak calling information.

For more details about samples refer to the Inspecting sample properties section. For details about settings and directory configuration refer to the Settings section.

6.4.1.8 Closing an experiment

You can close an experiment by clicking ✕ to the right of the experiment name, regardless of whether the experiment is active or not.

If the experiment was modified, the system asks you whether to save the changes or not.
Click "Yes" to save or "No" to discard the changes.
Select "Cancel" to cancel closing.

For more details about saving experiments, see the Saving an experiment section.

6.4.1.9 Importing BioCalculator Data

Data files from the BioCalculator Software (the QIAxcel software version prior to QIAxcel ScreenGel software) can be imported into the QIAxcel ScreenGel software.

Proceed as follows:

1. Select "Import BioCalculator Data" from the "File" menu.

Opening the "File" menu.

Note: This menu option is available in the "Analysis" environment only.

2. A dialog box appears enabling selection of the BioCalculator data files to be imported. Navigation starts initially with the most recently used BioCalculator import directory or the user's "My Documents" directory. Navigate to the directory that the BioCalculator data files will be imported from. Use the file type to filter.
3. Select the files to be imported from the list and click "Import" .

   Note: Only one file of type "**.hff**" can be imported at a time. The "**.hda**" files referred to by the selected "**.hff**" file are expected to be located in the same folder as the "**.hff**" file.

   Note: Change the file type to "**HDA**", to select multiple "**.hda**" files.
4. The files will be converted and displayed in the "Experiment Explorer".

   If a "**.hff**" file was selected, an experiment will be created containing as many rows and samples as in the "**.hff**" file. Repeats will be represented by separate plates.

   The experiment will be saved in the default experiment directory, as defined in the user settings.

   Note: If there are incomplete rows, the empty sample positions remain empty.

   Note: If a sample position is referred to multiple times, separate plates are also generated.

   Note: If there were experiments already loaded in the "Experiment Explorer", the newly opened experiment will be displayed as the last experiment, at the bottom). This experiment automatically becomes active.

Note: If the mode (DNA, RNA, or protein) of the selected files is different to the current mode, the files cannot be imported.

5. Visualize the samples.

   Note: To see the imported analysis parameters and reference marker table in the analysis parameters tab, right-click a sample in the experiment explorer, and select the context menu option "Transfer Analysis Instructions".

To load an experiment that was created with the QIAxcel ScreenGel software, use the "Load" function as described in the Loading sample data section.

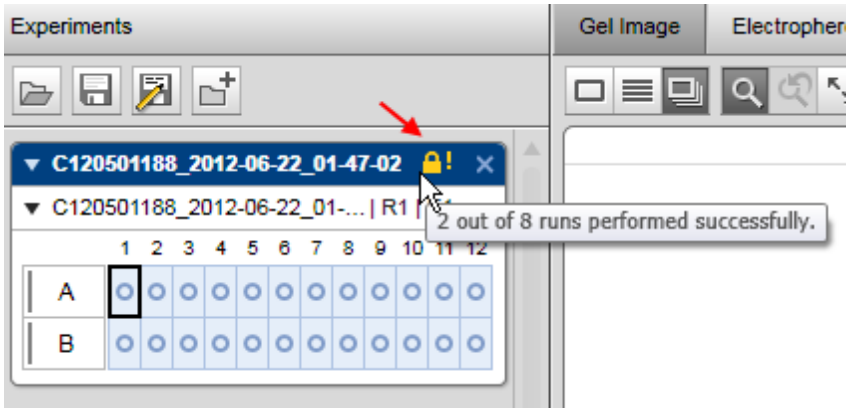
6.4.1.10 Revising sample information

To revise the sample information after the run, select the sample in the experiment explorer, right-click the sample, and select the context menu option "Revise Sample Information". Enter the new sample information in the dialog that appears.

Note: The context menu option "Revise Sample Information" is enabled only if the user has the right to revise the sample information. The administrator can grant the right in the User management.

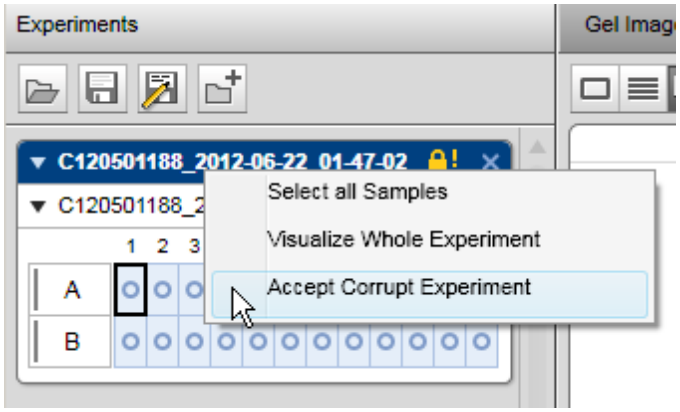
6.4.1.11 Handling an incomplete experiment

An experiment can be incomplete if the process stopped during data acquisition. This is indicated in the experiment explorer with a yellow lock icon. Hover with the mouse over the lock icon to display a tooltip with further information.



Incomplete experiment.

You can remove this icon from the experiment (for example, because you could successfully reprocess the missing runs). Right-click the experiment name and select the context menu option "Accept Corrupt Experiment".



Accept an incomplete experiment.

Note: This option is available only for users who have this right (based on their user role). The administrator can grant the right "May accept incomplete experiments" using the user management system.

The report will contain information about the incomplete process and the acceptance in the report overview section.

6.4.2 Viewing sample data

The "Analysis" environment offers several options for visualization of raw data and analysis results:

- A gel view, which can display several samples — see Gel view.
- A single electropherogram view, which visualizes a single sample along with its analysis results — see Electropherogram view.
- An electropherogram overview, which visualizes several electropherograms below each other — see Electropherogram overview.
- An electropherogram superposition view, which visualizes several electropherograms in one plot — see Electropherogram superposition view.

All views allow data exploration by zooming and scaling the data.

6.4.2.1 Adding samples to views

Note: A maximum of 97 samples can be visualized at a time in the gel view and electropherogram overview. If this limit is reached, visualization of more samples is disabled.

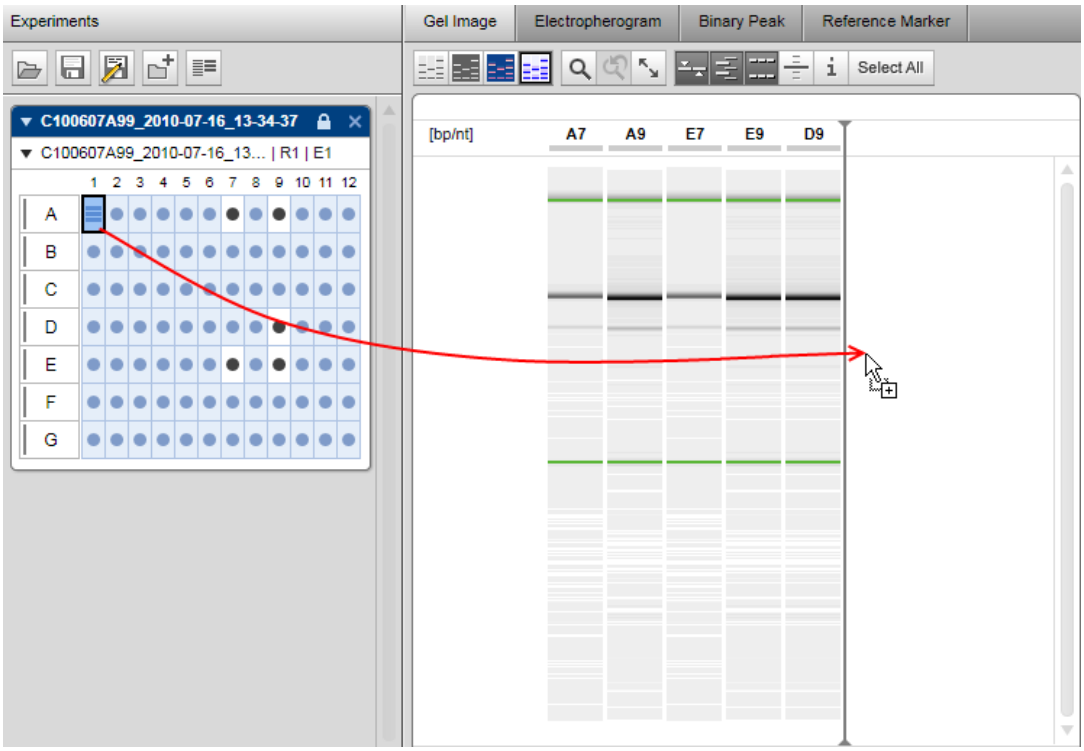
Samples can be added to a view by dragging samples from the "Experiment Explorer" to:

- The gel view
- The electropherogram overview
- The electropherogram superposition view (see description at the end of this section)

Proceed as follows:

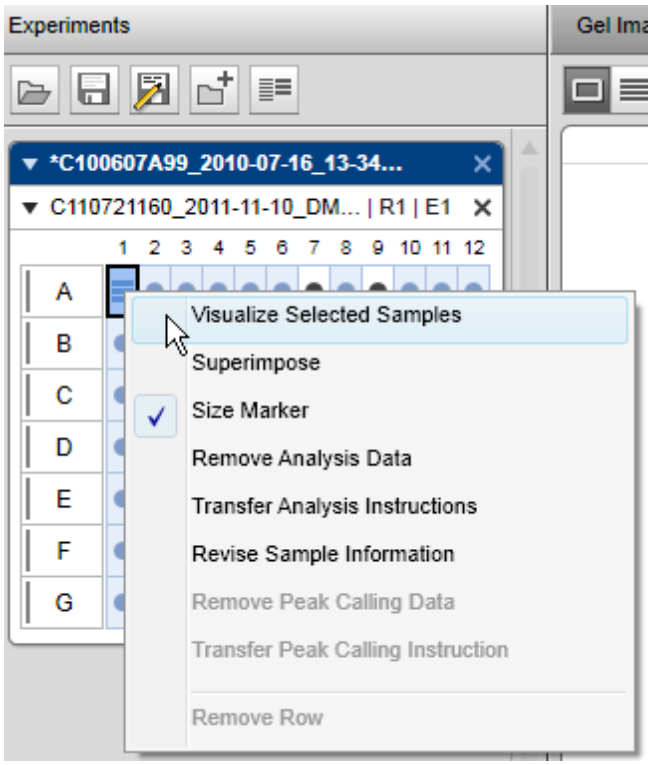
1. In the "Experiment Explorer" select the samples to be visualized.
2. Left-click the selected samples, drag to the view, and drop. All selected samples will be displayed in the view.

   Note: In gel view and electropherogram overview a marker is shown that indicates the position when dropping. All samples will be displayed at the selected position. See also Changing lane order.



Dragging sample A1 to the gel image, to the right of D9.

Alternatively, samples can be added to the views through the sample context menu of the experiment explorer. Use the "Visualize Selected Samples" option to add the selected samples to the views.



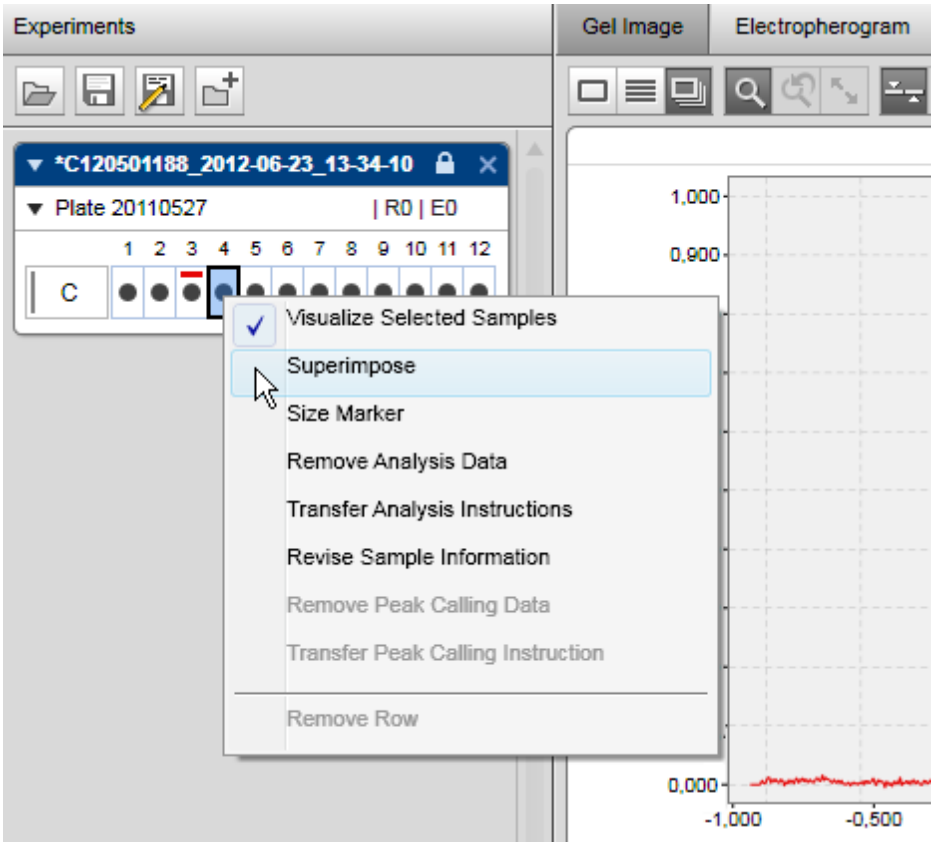
Visualize selected samples.

Finally, to visualize a **plate**, right-click the plate name and select the context menu option "Visualize Whole Plate". To visualize the **whole experiment**, right-click the experiment name and select the context menu option "Visualize Whole Experiment".

Unlike all other views, the superposition view does not automatically display all samples selected for visualization.

To add samples to the superposition view:

1. In the "Experiment Explorer" select the samples to be added.
2. Open the context menu of the selected samples in the "Experiment Explorer".
3. Select the "Superimpose" option.



Adding sample C4 to superposition.

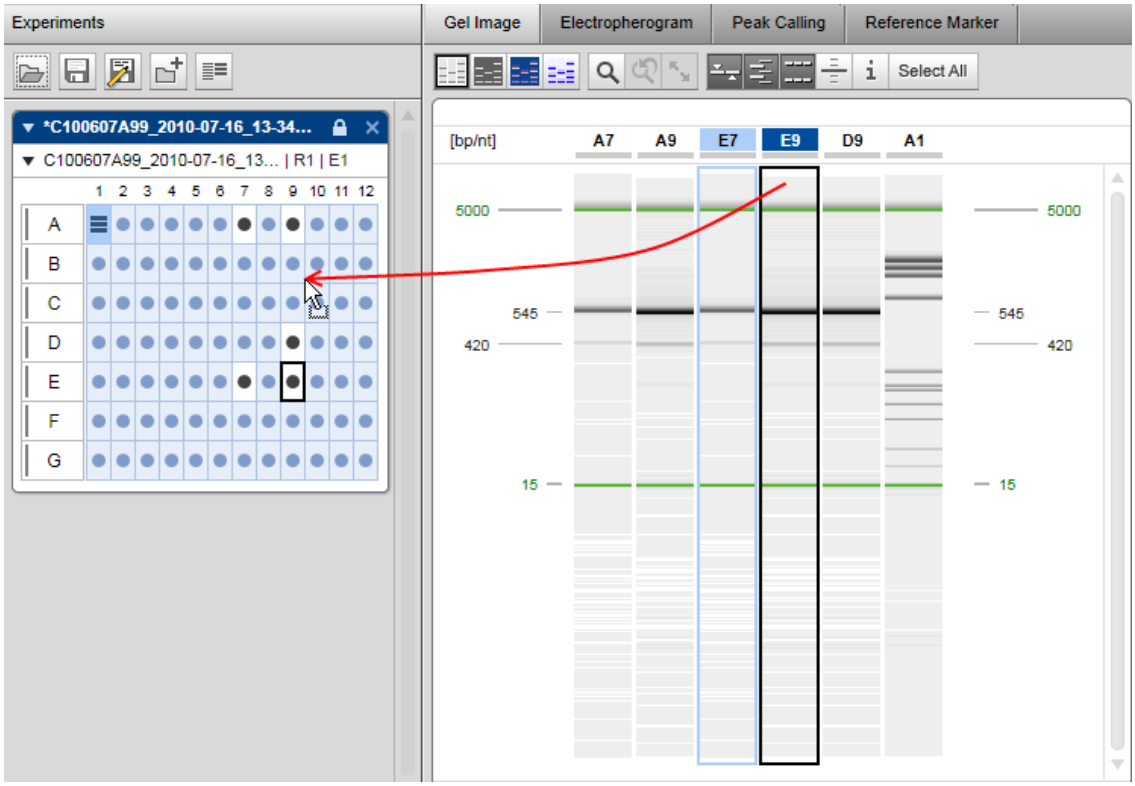
The selected samples will be added to the superposition view. In the "Experiment Explorer" all samples that are displayed in the superposition view are marked by a colored rectangular according to their color in the superposition.

Note: Up to 12 electropherograms can be superimposed. A warning will be displayed if the limit is exceeded.

Alternatively, drag-and-drop up to 12 selected samples from the "Experiment explorer" to the superposition view.

6.4.2.2 Removing samples from views

Samples can be removed from the views by dragging the selected samples from the view back to the "Experiment Explorer".

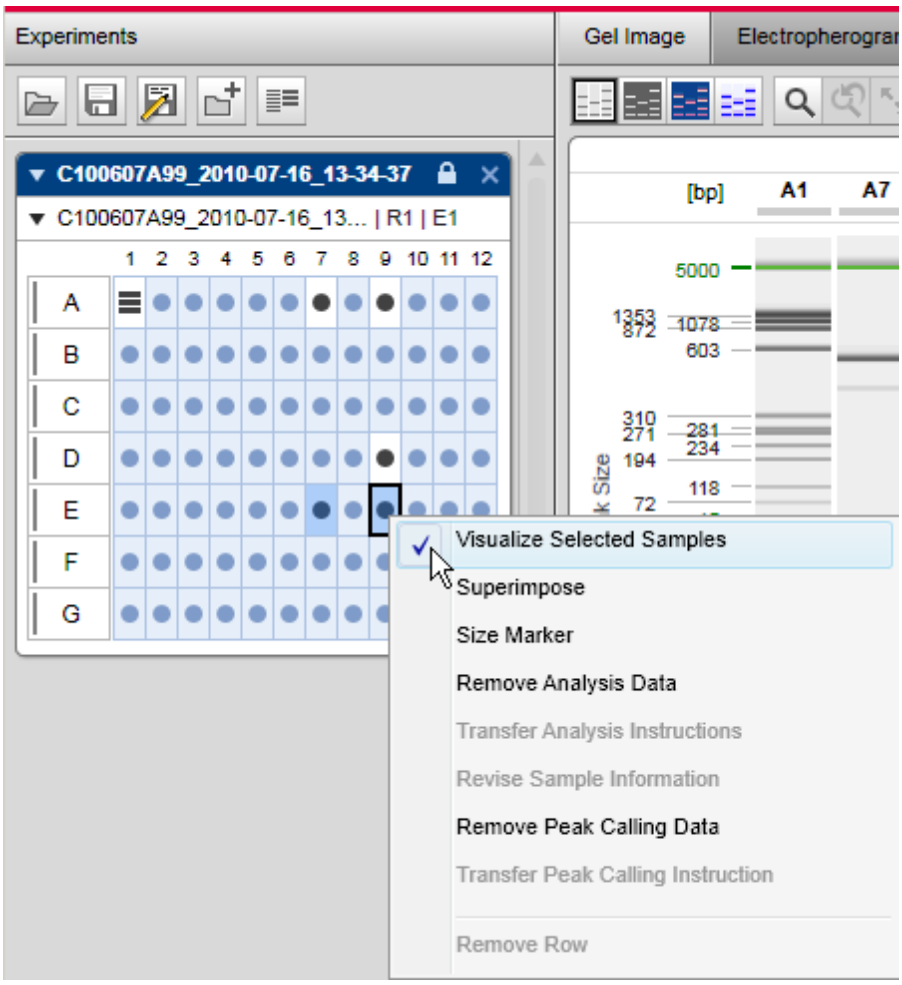


Removing samples E7 and E9 from the gel image.

Note: You can drop the samples elsewhere in the "Experiment Explorer".

Alternatively, use the context menu of the samples in the "Experiment Explorer":

1. Select the samples that should no longer be visualized.
2. Right-click a selected sample and uncheck the "Visualize Selected Samples" option to remove samples from the views.



Removing selected samples E7 and E9 via the context menu.

Finally, if a whole plate or a whole experiment is visualized, you can remove all the samples from the view. Right-click the plate name or the experiment name and uncheck the "Visualize Whole Plate" or "Visualize Whole Experiment" option from the appropriate context menu.

To remove samples from the superposition view, proceed as follows:

1. In the "Experiment Explorer" select the samples to be removed.
2. Open the context menu of the selected samples in the "Experiment Explorer".
3. Unselect the "Superimpose" option.

6.4.2.3 Exporting view to clipboard

Sample views can be copied to the clipboard.

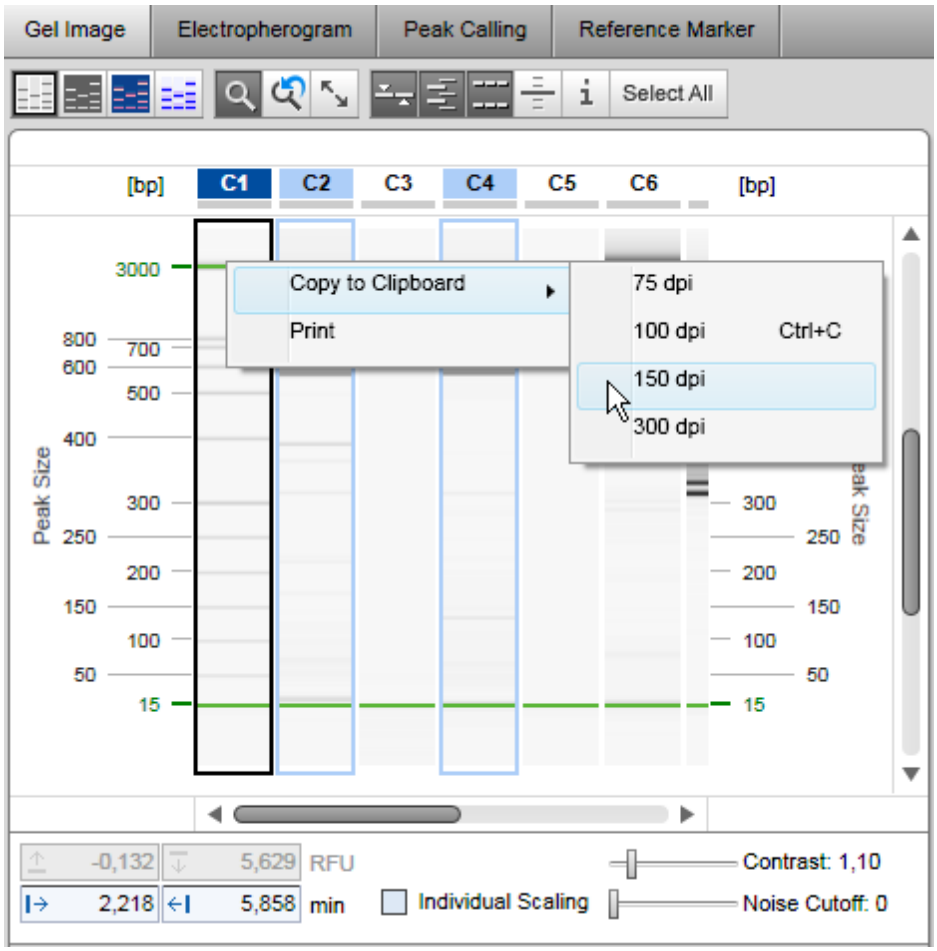
1. Select the lanes/electropherograms to be copied (in gel view or electropherogram overview).
2. Right-click the selected sample and select from the menu item "Copy to clipboard" the resolution you want have the image with.
3. Switch to the application you want the view to appear in and paste.

Note: You can use the keyboard shortcut Ctrl+C to copy selected images to clipboard. Keep in mind that using of key shortcut applies the default resolution value (96 dpi), not the last used one.

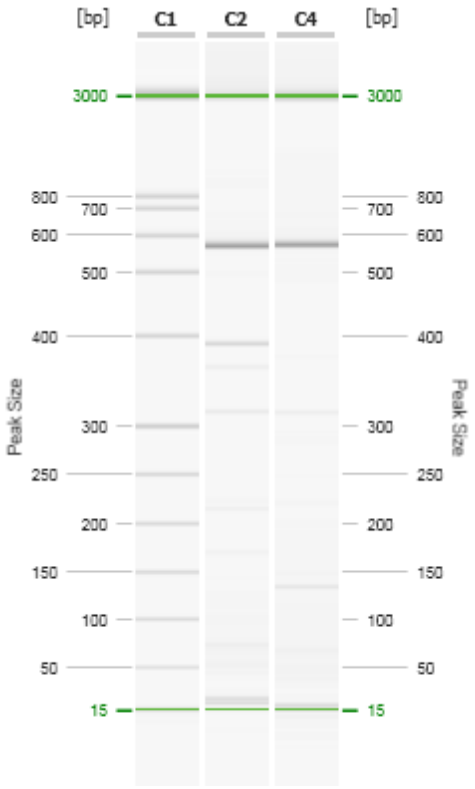
Note: When you paste the image in an application, make sure that it uses the right resolution. QIAxcel ScreenGel puts the pixel array on clipboard which adapted for desired resolution (this means that the image has the appropriate pixel size). The application you paste the image in, shall be able to interpret this information correctly.

Note: The samples that have been copied to clipboard, have the same image settings as in the visualization view (such as color palette, contrast, noise cutoff, and zoom factor).

Note: In the single electropherogram view and electropherogram superposition view the gel lane and C-channel diagram will be copied to clipboard too if they are displayed in visualization. If you hide both gel lane and C-channel diagram, only samples will be copied to clipboard. You can access the "Copy to clipboard" popup menu from gel lane and C-channel diagram as well.



Copying the gel image of the selected samples C1, C2, and C4 to the clipboard.



C1, C2, and C4 pasted.

6.4.2.4 Direct printing view

You can directly print images of selected samples:

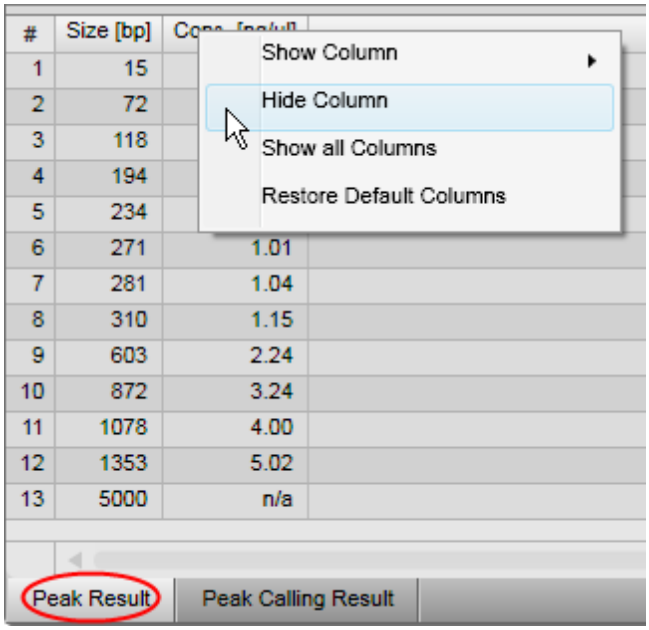
1. Select the lanes/electropherograms to be printed.
2. Right-click the selected sample and select the context menu item "Print".

This function works in a similar way to the 'copying to clipboard' function with default image resolution; the selected samples will be sent to the default printer. They have the same image settings as in the visualization view (such as contrast, noise cutoff, and zoom factor).

The image sent to the printer is identical to the image you would copy to the clipboard; if the gel lane and C-channel diagram are displayed in the single electropherogram view and electropherogram superposition view, they will be printed as well.

6.4.2.5 Result table

The analysis result table of a sample is displayed in the "Analysis" environment below the electropherogram views or the gel view. When an analyzed sample is selected, the results are shown in the result table. The displayed columns depend on the mode.



DNA result table.

The "Peak Result" table lists the detected peaks of the sample. Refer to the Peak result columns section for detailed information on available peak properties.

The "Peak Calling Result" table lists the peak calling result of the sample. Refer to the Peak Calling section for detailed information.

Modifying the result table

The information displayed in the result table can be customized for the electropherogram single view and overview independently. The customization applies to all further viewing of the results.

Note: In the electropherogram superposition view, a small non-customizable result table is displayed.

Adding a column

To add a column:

1. Right-click the table header.
2. Select the column to be displayed from the "Show Column" selection.

Note: Select the "Show all Columns" option to display all columns. Select the "Restore Default Columns" option to display the default for the application.

Removing a column

To hide a column:

1. Right-click the column header.
2. Select the "Hide Column" option from the context menu.

Changing column order

The order of the displayed columns can be changed by dragging a column header to the desired position. While dragging, a marker is displayed that indicates the position of the column when dropping it.

Resizing column width

The column width can be changed by dragging a vertical cell border in the table header.

Interacting with the result table

Selecting and removing a peak

When selecting a peak in the result table, the peak is highlighted in the electropherogram (single electropherogram view and electropherogram overview). To select a peak in the result table, left-click the peak number in the "#" column. To unselect the peak, use the context menu option "Unselect Peak" or just click to another cell. To remove the selected peak from the result table, use the context menu option "Delete Selected Peak".

Exporting analysis results

The contents of the result table can be exported to other applications using the Windows clipboard. There are several ways to select the table cells:

- Select the cells with the mouse while holding down the left mouse button.
- Click the first column of a row to select a row. You can also select multiple columns using the "Shift" and "Ctrl" key.
- Click the column header to select a column.
- Click the column header of the first column to select all cells.

To copy your selection:

1. Select cell(s).
2. Right-click a selected cell.
3. Click the "Copy selected cells to clipboard".
4. Paste the data to other applications, for example, Microsoft Excel.

Note: The result data are exported using the local settings of the Windows system. Make sure that the target application also uses the local settings to interpret the numbers.

Peak result columns

The following columns are available:

#	Number of peaks in the sample.
Size [bp]	For DNA mode only. Fragment size in base pairs.
Size [nt]	For RNA mode only. Fragment size in nucleotides.
m [kD]	For protein mode only. Molecular mass of the protein in kilodalton (kD).
Conc. [ng/µl]	For DNA and RNA mode only. Concentration of the fragment in ng/µl.

	Note: This value is not calculated for alignment marker peaks.
Rel. Conc. [ng/µl]	For Protein mode only. Relative concentration of the protein in ng/µl. **Note:** Rel. concentration is calculated by referring the sample peaks to a defined peak of the size marker. The concentration can only be given as relative concentration since the binding of the dye differs from one protein species to another. **Note:** This value is not calculated for alignment marker peaks.
Mol. [nmol/l]	For DNA and RNA mode only. Molar concentration (molarity) in nmol/l. The calculation is based on the fragment size and concentration. **Note**: This value is not calculated for alignment marker peaks.
Saturated	Indicator whether the peak intensity reaches the maximum possible intensity (see Saturated Signals section). The calculated height, area and concentration of saturated peaks are not correct.
S/N	Signal-to-noise ratio of the peak. The noise is approximated with three times the standard deviation of the noise data points from the baseline.
NA	Normalized area, also called corrected peak area. This is the peak area divided by the migration time of the peak apex.
Area	Peak area (integration of the area under the signal and above the baseline).
NA %	Normalized peak area relative to the sum of all normalized peak areas. **Note:** This value is not calculated for alignment marker peaks.
Ratio NA	The area ratio with respect to the previous peak. The alignment marker peaks and the first data peak in the table will have an empty field here.
Height	Height of the peak at its maximum.
Height %	Peak height relative to the sum of all peak heights. **Note:** This value is not calculated for alignment marker peaks.
Res.	The separation resolution with respect to the previous peak. The first peak in the table will have an empty field here.
FWHM [sec]	The peak width at half the maximum intensity (full width at half maximum), which is a parameter for peak resolution and thus the precision of size calculation.
Start [min]	Start time/X-value of the peak in minutes.
Time [min]	Time/X-value for the peak maximum.
Stop [min]	Stop time/X-value of the peak in minutes.
Rel. Time	Relative time/X-value for the peak maximum. This value is mode-dependent: In DNA and protein mode, the relative position of the peak between lower alignment marker and upper alignment marker is mapped to the interval from zero to one, i.e. all peaks have a Rel. Time between zero and one. The alignment markers have a Rel. Time of zero and one, respectively.

In RNA mode, the relative position of the peak in relation to the lower alignment marker is calculated, i.e. the alignment marker has a Rel. Time of 1 and all other peaks have Rel. Time higher than one.

6.4.2.6 Gel view

The gel view displays the gel images of the samples.

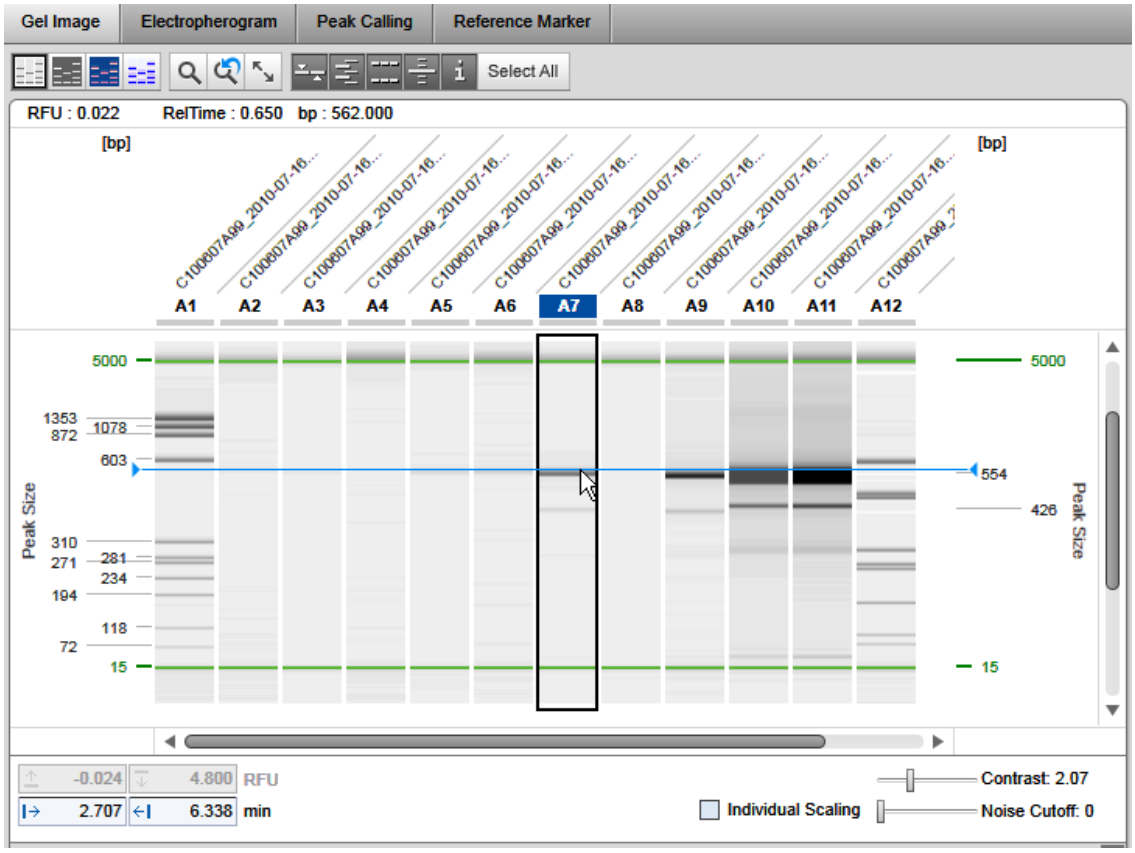
The lanes in the gel view can be displayed in four view modes:

Normal mode

Inverted mode

False color rendering mode

Coomassie mode (default mode for protein)



Gel view with ruler, sample labels, and peak annotation.

The y-axis on the left-hand side is the main scale for the whole image. When the size scale is selected, it is based on the bands of the reference marker applied to all samples (see sample A1 in the image above).

The y-axis on the right-hand side describes the detected bands of the selected sample only (see above: highlighted with the black border, in the image above sample A7). It is available in the application only, not in report/export images (also not if the "Use Images as Displayed" option is selected).

Above each gel image the sample position is displayed (e.g. A1, A2, and so on). For a gel image a tool tip can be displayed by moving the mouse pointer to the sample number. This tool tip has information about the plate, the number of the run, and method that the sample was processed with.

If the mouse pointer hovers over the gel lanes, the values at the current cursor position are shown in the upper left corner of the view.

To view a sample in detail, double-click its gel lane. The view changes to single electropherogram view. To return to the gel view, select the "Gel Image" tab again.

You can interact with the gel view mainly through the buttons above the view:

Toggles zoom mode on/off.

In zoom mode (button pressed), the mouse is used to select a region for zooming into ("rubber band" function — see General software usage). In addition, you can use the scroll wheel of the mouse to zoom in and out.

If this button is not pressed, the drag-and-drop function is activated to change the lane order.

Note: The controls in the lower left corner of the gel view can be used to set the zoom region to absolute values, independently of the zoom mode.

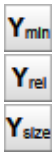
Note: The drag-and-drop function is always possible if the mouse cursor is over the gel lane label, even in the zoom mode (button pressed).

Auto scale.

Resets the zoom region to the overall data range, undoing all zooming.

Undo zoom.

Returns to the previous zoom state.



Toggles the unit of the y-axis scale on the **left-hand side** of the gel view.

Left-click the button to switch to the next unit.

If the button text is "Yrel", the y-axis on the left-hand side will display the relative migration time. If the button text is "Ysize", the y-axis on the left-hand side will display the size (in bp, nt, or kD, respectively). In both cases, the displayed samples will be aligned according to the alignment markers. Aligning the samples facilitates the comparison of sample peak positions.

If the button text is "Ymin", the y-axis will display absolute migration time on the left-hand side of the gel view, and the samples will not be aligned.

Note: The alignment is only possible if all visualized samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the relative time/size scale cannot be created, and a message will be shown instead. In this case, toggle the button to use the absolute time scale, reanalyze the samples so that the alignment markers have been correctly identified, or remove from the view the samples that have a different alignment marker, or those samples for which alignment markers could not be correctly identified.

Note: The status of the button does not change when switching to an electropherogram view.

Toggles the unit of the y-axis scale on the **right-hand side** of the gel view.

If the button is pressed, the y-axis displays a size scale on the right-hand side of the gel view, based on the detected bands of the currently selected sample (with the black border).

If the button is not pressed, the y-axis on the right-hand side displays a relative time scale.

Note: The relative time scale is only possible if the sample has been analyzed and the alignment markers have been correctly identified. Otherwise, the relative time scale cannot be created, and a message will be shown instead. The size scale is only possible if, additionally, the sample has been analyzed with a reference marker table. Otherwise, the size scale cannot be created, and a message will be shown instead.

Note: The status of the button (pressed/not pressed) does not change when switching to the single electropherogram view.

Toggles highlighting the alignment marker bands in green.

Note: The highlighting is only possible for analyzed samples if the alignment markers have been correctly identified.

Toggles a horizontal ruler at cursor position.

Toggles the sample labels. The labels appears above the lanes, diagonal oriented for the better readability.

Controls for contrast settings are located below the gel view to the right. The functions are described below.

Individual scaling	When the checkbox is unchecked (which is the default, when starting the QIAxcel ScreenGel), the colors are adapted to the overall maximum signal height of all samples. Use this option for comparison of samples. When the checkbox is checked, the colors are adapted to the maximum signal height of each individual sample. If the samples differ greatly in sample intensity, use this option. Changing the option applies to further display of gel views for all experiments.
Contrast	Use the slider to change the contrast according to your needs. The contrast value will be saved together with the experiment. Thus, you can customize the gel images independently of other experiments.
Noise cutoff	Use the slider to customize display of the noise in the signal. Move the slider to the extreme left position to see all signals. Move the slider to the right to suppress small signals, eliminating the noise. As contrast, the noise cutoff value will be saved together with the experiment.

Changing lane order

The gel lanes can be reordered by drag-and-drop. The lane order takes effect for all views where the samples are visualized. The changed order will be saved when saving the experiment.

To change the lane order:

1. Select one or more lanes in the gel view.
2. Left-click the header of the selected lane or lanes and drag it to the new position. While dragging, a marker is shown indicating the new position of the lane(s) when dropping.
3. Drop the lane(s) when the marker indicates the correct new position. The lane(s) will be placed in that position. If more than one lane was selected, the lanes will be inserted in the same order as they were in before.

Note: If the zoom button is toggled off, dragging can start also inside a gel lane.

6.4.2.7 Electropherogram view

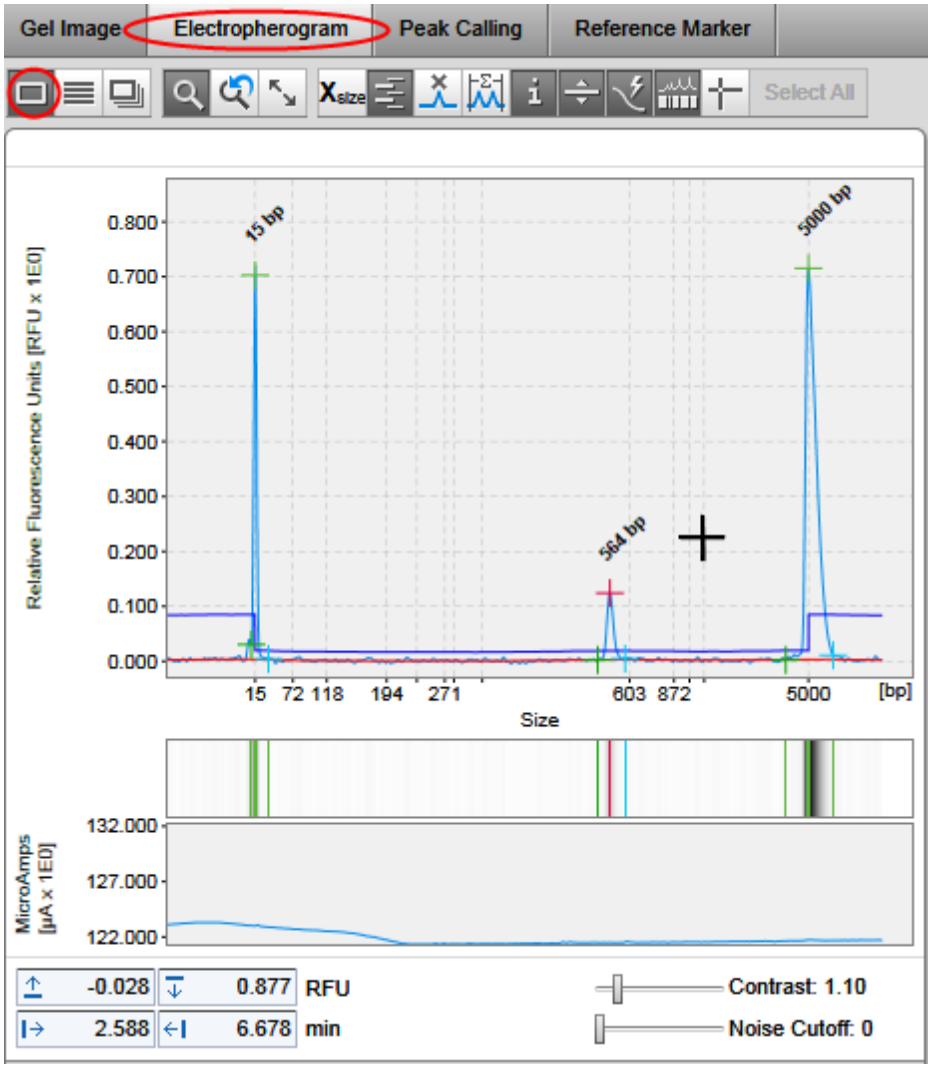
The electropherogram view is activated by clicking on the "Electropherogram" tab in the analysis environment. Three electropherogram views can be selected using the following buttons in the tool bar:

Single electropherogram view.

Overview mode with several single electropherograms.

Superposition view with several superimposed electropherograms.

The single electropherogram view is described in this section. The overview and superposition mode are described in the following sections.



Single electropherogram with peak annotation and displayed electrical current.

The single electropherogram view consists of a plot showing the recorded signal and the gel representation of the signal below the main plot.

Controls for the zoom region size and contrast settings of the gel view are located below the graphical representations of the signal. The current cursor position is shown in the upper left corner of the view.

You can mainly interact with the electropherogram through the buttons in the tool bar (all buttons in this table are listed in "not pressed" state, left-click the button to press/release):

Toggles zoom mode on/off. For details see Zooming and scaling.

Auto scale. For details see Zooming and scaling.

Undo zoom. For details see Zooming and scaling.

Insert peak. For details see Adding a peak.

Manual integration of a time range. For details see Manual range integration.

Toggle the unit of the x-axis.

Left-click the button to switch to the next unit. If the button text is "Xmin", the x-axis displays the absolute migration time. If the button text is "Xrel", the x-axis displays relative migration time. If the button text is "Xsize", the x-axis displays the size (in bp, nt, or kD, respectively).

Note: The relative time scale is only possible for an analyzed sample for which the alignment markers have been correctly identified. The size scale is only possible if, additionally, the sample has been analyzed with a reference marker.

Note: The status of the button does not change when switching to another electropherogram view or to gel view.

Toggles (shows/hides) peak labels above the apex of each peak.

Note: Only those peak labels are displayed, that do not overlay an adjacent label. Hover the mouse cursor over the peak apex to get a tool tip with the peaks label.

Toggles the peak label units.

If the button is pressed, the peak labels display the peak size (in bp, nt, or kD, respectively). If the button is not pressed, the peak labels display absolute or relative migration time, according to the x-scale.

Note: The size unit is only possible for analyzed samples, where a size determination was performed (for details refer to Size and Concentration determination). If the size of the peaks was not determined, "n/a" is displayed instead.

Note: The status of the button (pressed/not pressed) does not change when switching to gel view.

Toggles (shows/hides) the peak threshold (displayed in blue).

The threshold parameter can be interactively changed by moving the threshold with the mouse. For details, see Modifying the threshold.

Toggles gel lane.

When the button is clicked, the gel representation will be shown below the electropherogram in alignment with the x-axis.

Toggles electrical current.

When the button is clicked, the diagram displaying the electrical current measured during data acquisition will be shown below the gel representation according to the x-axis.

Toggles ruler.

Activates vertical and horizontal rulers used to compare peak heights and positions.

Below the gel view at the right, controls for contrast settings are located. The controls are described below.

Contrast	Use the slider to change the contrast according to your needs. Contrast changes apply for further display of the electropherogram single view for all experiments, but do not affect the contrast settings of the gel view.
Noise cutoff	Use the slider to customize display of the noise in the signal. Move the slider to the extreme left position to see all signals. Move the slider to the right to suppress small signals, eliminating the noise. As for contrast, changes to the noise cutoff value do not affect the settings of the gel view.

Zooming and scaling

The "Electropherogram" view allows exploration of the data via zooming and scaling.

Toggles zoom mode on/off.

When the button is clicked, the mouse is used to select a region for zooming into. For information about how to use the "rubber band" function, see General software usage. Additionally, you can use the scroll wheel of the mouse to zoom in and out.

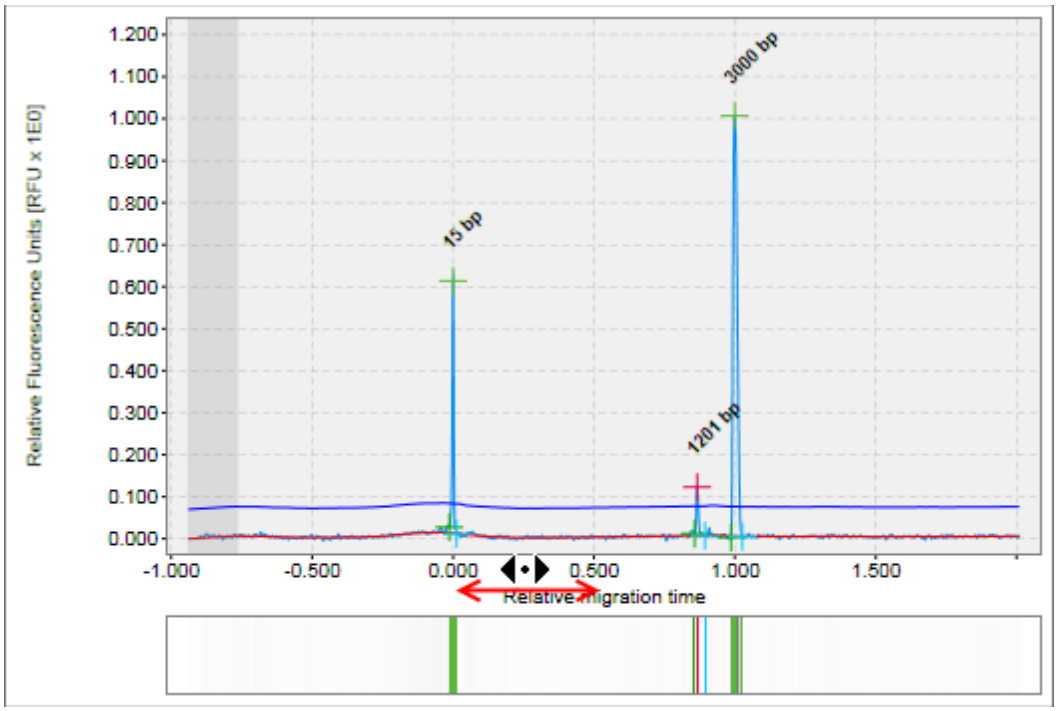
Auto scale.

Resets the zoom region to the overall data range (both in time and RFU dimension), undoing all zooming.

Undo zoom.

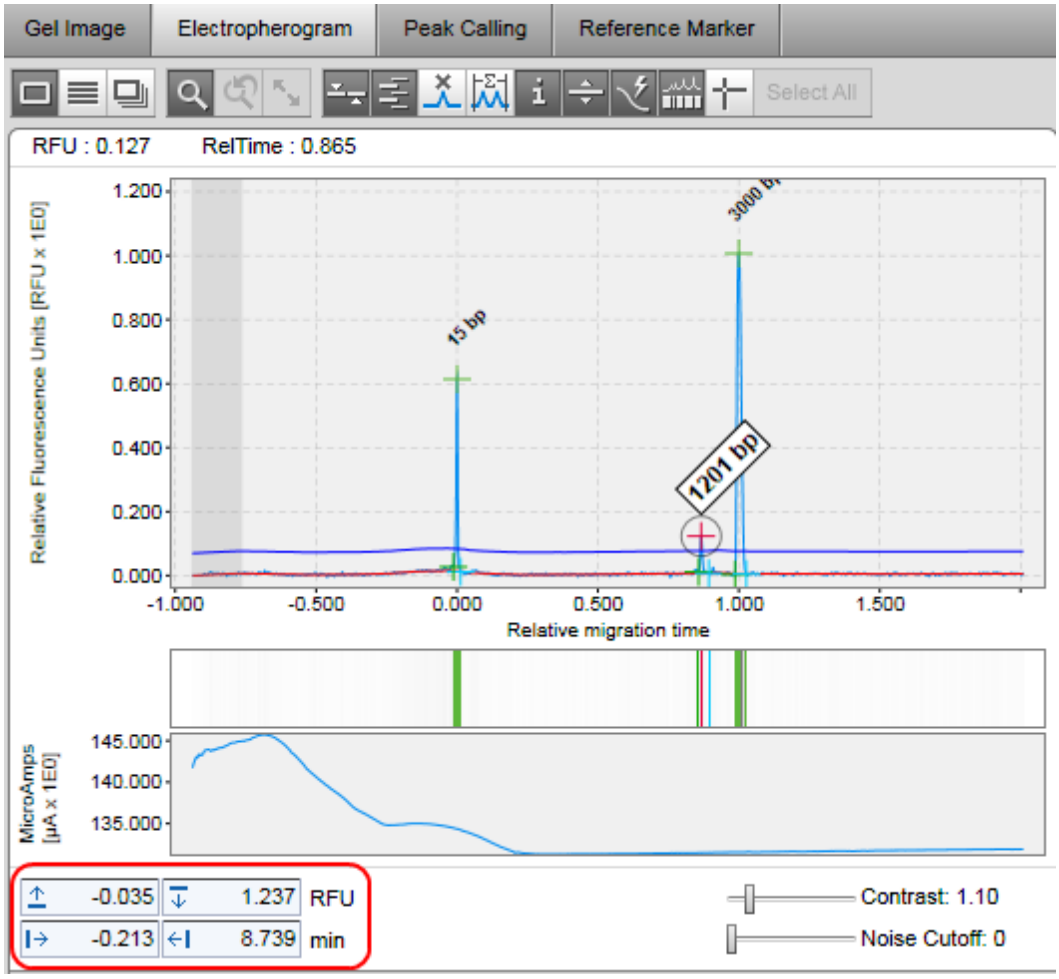
Returns to the previous zoom state.

Independent of the zoom mode, all electropherograms can be panned using the axes. You can shift the zoom region horizontally by dragging the x-axis. To shift the zoom region horizontally drag the y-axis.



Dragging the x-axis.

In addition to the tool buttons, the controls in the lower left corner of the "Electropherogram" view can be used to set the zoom region to absolute values.



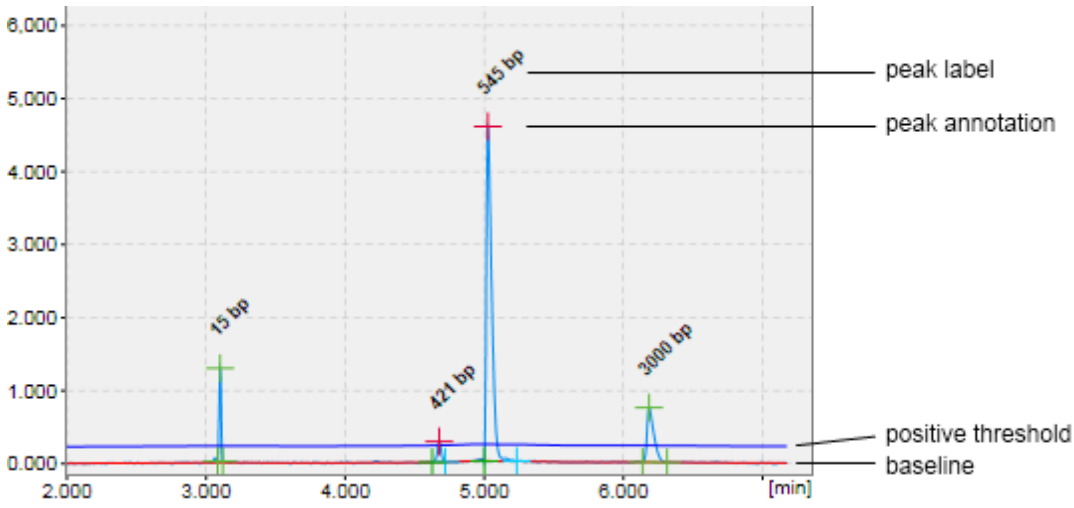
Input fields to set the zoom region to absolute values.

Note: For RFU values, only the values are permitted that are inside of the actual values. The values lying outside of the range of actual values range are not accepted and the background of the input field becomes yellow.

Note: For time values, the input of the upper range value up to an hour is allowed.

Peak annotations

In an analyzed sample the analysis result is displayed along with the raw signal. Each peak has peak markers for start (green), apex (red, green for alignment marker peaks), and stop (turquoises).



Peak annotations

The unit of the peak label depends on the "Toggle alignment" and the "Toggle unit of peak" buttons. For details, refer to Electropherogram view.

In addition to the peaks, the detected baseline (displayed in red) and the threshold for peak detection above the baseline (displayed in blue) are shown in the electropherogram.

Interacting with the result table

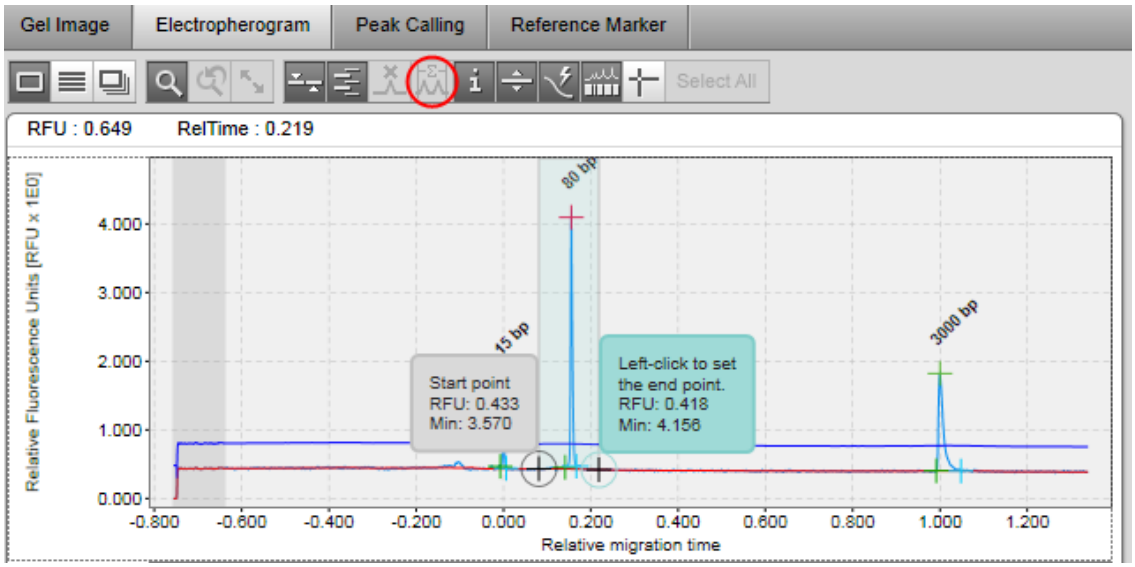
The functions are described below.

Selecting a peak	In the electropherogram, left-click the apex marker of the peak. Alternatively, in the result table, left-click the peak number in the "#" column. The peak will be marked with a red circle in the electropherogram and highlighted in the result table.
Selecting a peak	In the electropherogram, left-click the apex marker of the peak. Alternatively, in the result table, left-click the peak number in the "#" column. The peak will be marked with a red circle in the electropherogram and highlighted in the result table.
Unselecting a peak	In the electropherogram or in the result table, open the context menu of the selected peak and select the "Unselect Peak" option. The red circle in the electropherogram disappears as well as the highlighting in the result table.
Adding a peak	See Adding a peak for information about how to add a peak. The peak will be added to the result table.
Deleting a peak	See Deleting a peak for information about how to delete a peak. The peak will be removed from the result table, and the markers of the peak in the electropherogram disappear.

Manual range integration

The manual integration of a time range is possible using the range integration tool ( ).

After clicking the "Range Integration" button, you need to specify a region. To do so, first click the left border of the region, then click the right border of the region.



Selection of a region for manual integration.

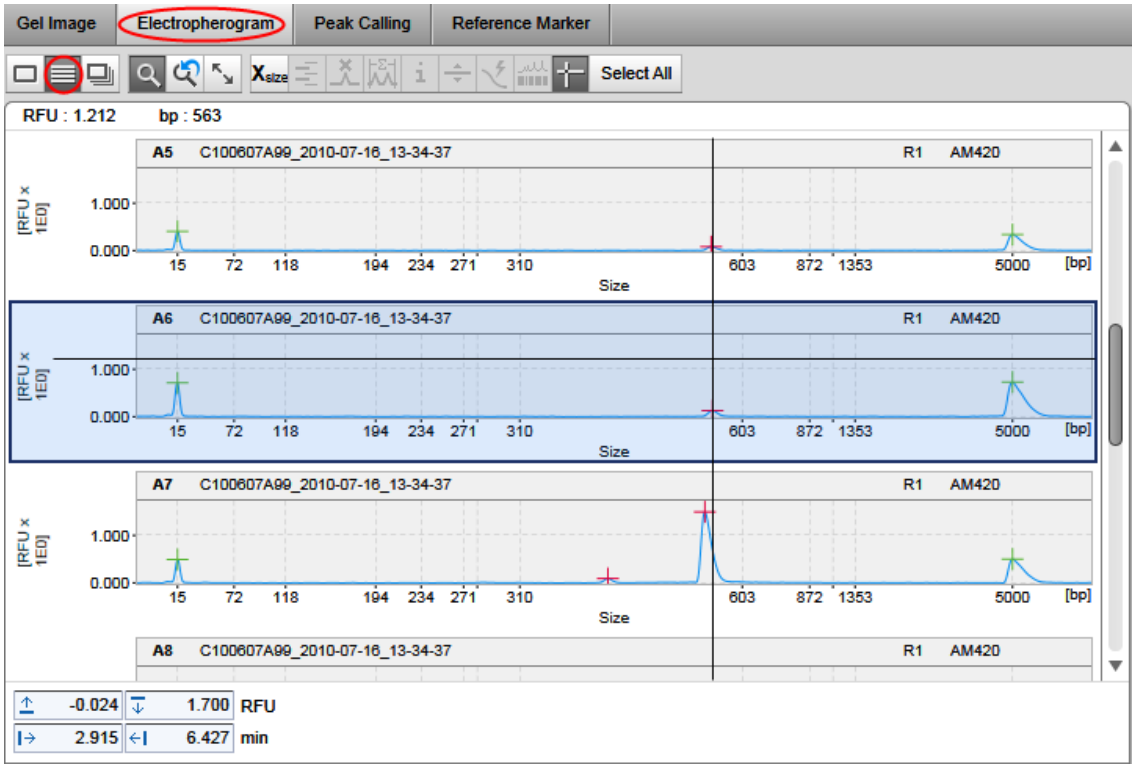
After selecting the region, a dialog box is displayed which shows the selected time range borders, the normalized area sum of the region, and the percentage of normalized area in relation to the overall normalized area.

Note: The calculated values can be copied to the clipboard using the context menu of the dialog box.

Note: The alignment marker peaks are not included in the normalized area calculation.

6.4.2.8 Electropherogram overview

The electropherogram overview displays several electropherograms one below the other. It is intended for an overview inspection of the acquired data. In the electropherogram overview the ruler tool is especially useful. It provides a means to compare peak positions between several samples, both for alignment marker peaks and sample peaks. For analyzed samples, each peak has a peak marker for apex time (sample peaks are red, alignment marker peaks are green).



Overview after analysis using the ruler tool.

In the analyzed samples, each detected peak has a peak marker for apex (red, green for alignment marker peaks).

The zooming and scaling functionality is very similar to the single electropherogram view (see Zooming and scaling). The only difference is that zooming affects all electropherograms.

Navigate using the scrollbar or arrow keys. To inspect an electropherogram in detail, double-click it.

The view changes to single electropherogram view. To return to the overview, click again.

You can interact with the electropherogram mainly through the buttons in the tool bar:

Toggles zoom mode on/off. For details see Zooming and scaling.

Auto scale. For details see Zooming and scaling.

Undo zoom. For details see Zooming and scaling.

Toggle the unit of the x-axis.

Left-click the button to switch to the next unit.

If the button text is "Xrel", the x-axis will display the relative migration time. If the button text is "Xsize", the x-axis will display the size (in bp, nt, or kD, respectively). In both cases, the displayed samples will be aligned according to the alignment markers. Aligning the samples facilitates the comparison of sample peak positions.

If the button text is "Xmin", the x-axis will display absolute migration time, and the samples will not be aligned.

Note: The alignment is only possible if all visualized samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the relative time/size scale cannot be created, and a message will be shown instead. In this case, toggle the button to use the absolute time scale, reanalyze the samples so that the alignment markers have been correctly identified, or remove from the view the samples that have a different alignment marker or those samples for which alignment markers could not be correctly identified.

Note: The status of the button does not change when switching to another electropherogram view or to gel view.

Toggles ruler.

Activates vertical and horizontal rulers used to compare peak heights and positions.

Changing order

The order of the electropherograms can be changed by dragging and dropping. The changed order is valid for all views for which the samples are visualized. The changed order will be saved when saving the experiment.

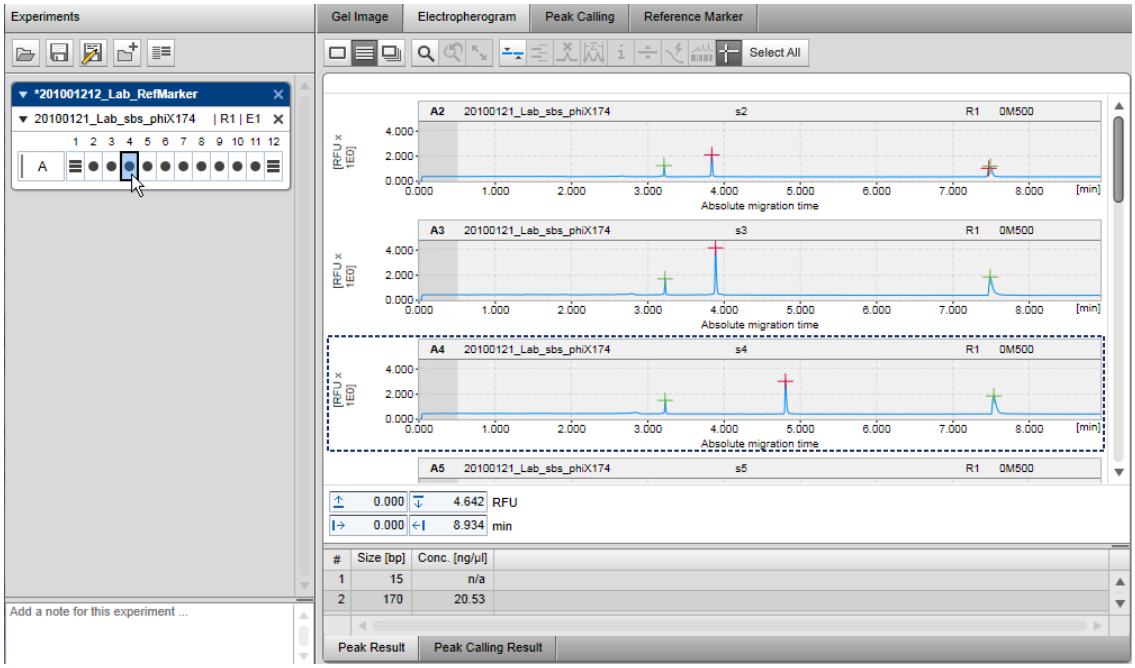
To change the order:

1. Select one or more electropherograms in the gel view.
2. Drag the selected electropherogram(s) to the new position. While dragging, a marker is shown indicating the new position of the electropherogram(s) when dropping.
3. Drop the electropherogram(s) when the marker indicates the correct new position. The electropherogram(s) will be placed at that position. If more than one electropherogram was selected, the electropherograms will be inserted in the same order as they were before dragging.

Note: To be able to reorder the electropherograms the zoom button must be toggled off.

Interacting with the result table

Below the electropherogram overview, the result table of one sample is displayed. This sample is marked in the "Experiment Explorer" with a dotted black border (see sample A4 in the image below). Select the sample in the "Experiment Explorer" or in the electropherogram overview by left-clicking it to view its result table.



Inspecting result table of sample A4.

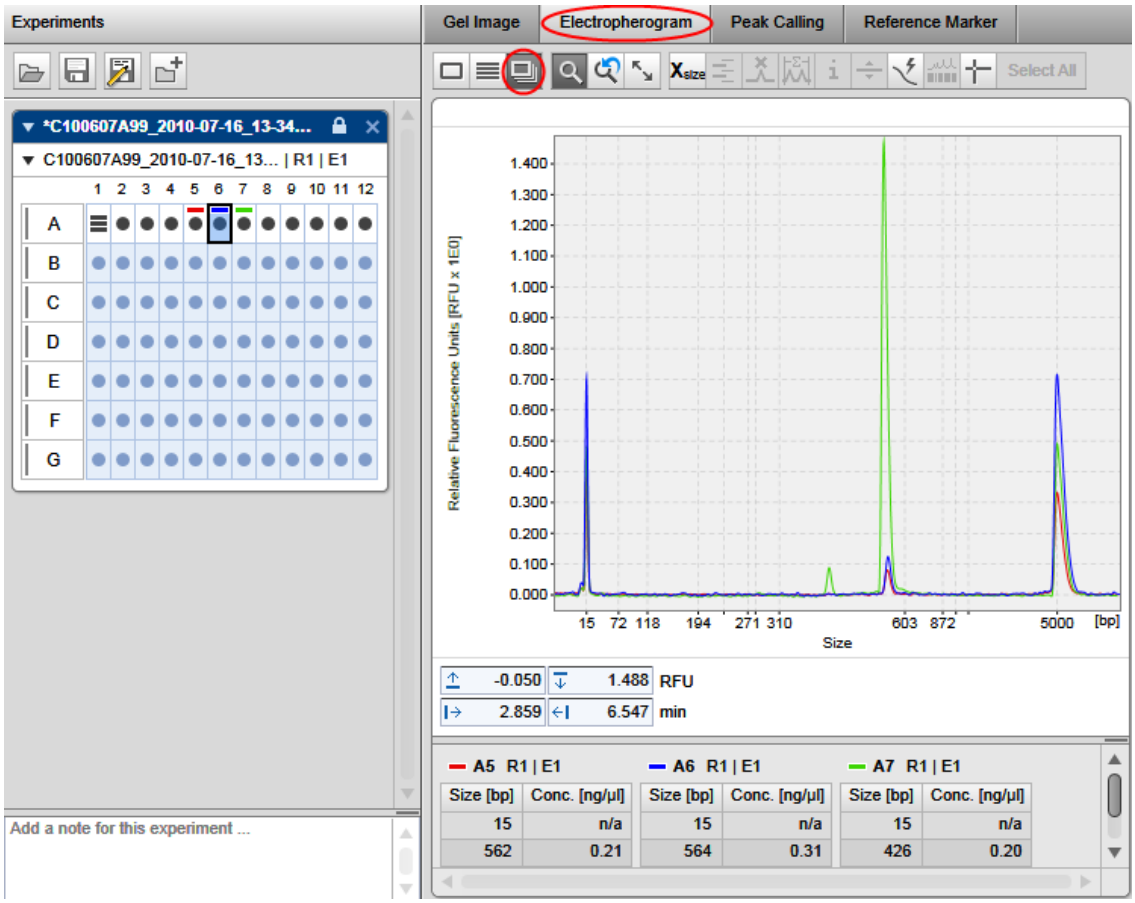
The functions are described below.

Selecting a peak	In the electropherogram, left-click on the marker of the peak apex. Alternatively, in the result table, left-click the peak number in the "#" column. The peak will be marked with a red circle in the electropherogram and highlighted in the result table.
Unselecting a peak	In the result table, open the context menu of the selected peak and select the "Unselect Peak" option. The red circle in the electropherogram disappears as well as the highlighting in the result table.
Deleting a peak	Select the peak to be deleted in the result table. Open the context menu of the result table and select the option "Delete selected peak". The peak will be removed from the result table, the marker of the peak in the electropherogram overview disappears.

6.4.2.9 Electropherogram superposition view

The electropherogram superposition view displays up to 12 electropherograms in one plot. It allows an easy comparison of several measurements.

In order to make the signals from different samples distinguishable, each sample has a distinct color.



Electropherogram superposition view.

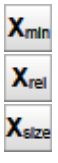
In the lower part of the superposition view, small result tables of all samples are shown along with the corresponding colors. The order of the result tables is the same as the sample order in the gel view or electropherogram overview.

You can interact with the electropherogram through the buttons in the tool bar:

Toggles zoom mode on/off. For details see Zooming and scaling.

Auto scale. For details see Zooming and scaling.

Undo zoom. For details see Zooming and scaling.



Toggle the unit of the x-axis.

Left-click the button to switch to the next unit.

If the button text is "Xrel", the x-axis will display the relative migration time. If the button text is "Xsize", the x-axis will display the size (in bp, nt, or kD, respectively). In both cases, the displayed samples will be aligned according to the alignment markers. Aligning the samples facilitates the comparison of sample peak positions.

If the button text is "Xmin", the x-axis will display absolute migration time, and the samples will not be aligned.

Note: The alignment is only possible if all visualized samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the relative time/size scale cannot be created, and a message will be shown instead. In this case, toggle the button to use the absolute time scale, reanalyze the samples so that the alignment markers have been correctly identified, or remove from the view the samples that have a different alignment marker or those samples for which alignment markers could not be correctly identified.

Note: The status of the button does not change when switching to another electropherogram view or to gel view.

Toggles electrical current.

When the button is pressed, the diagram displaying the superimposed electrical current measured during data acquisition will be shown below the electropherogram superposition according to the x-axis.

Toggles ruler.

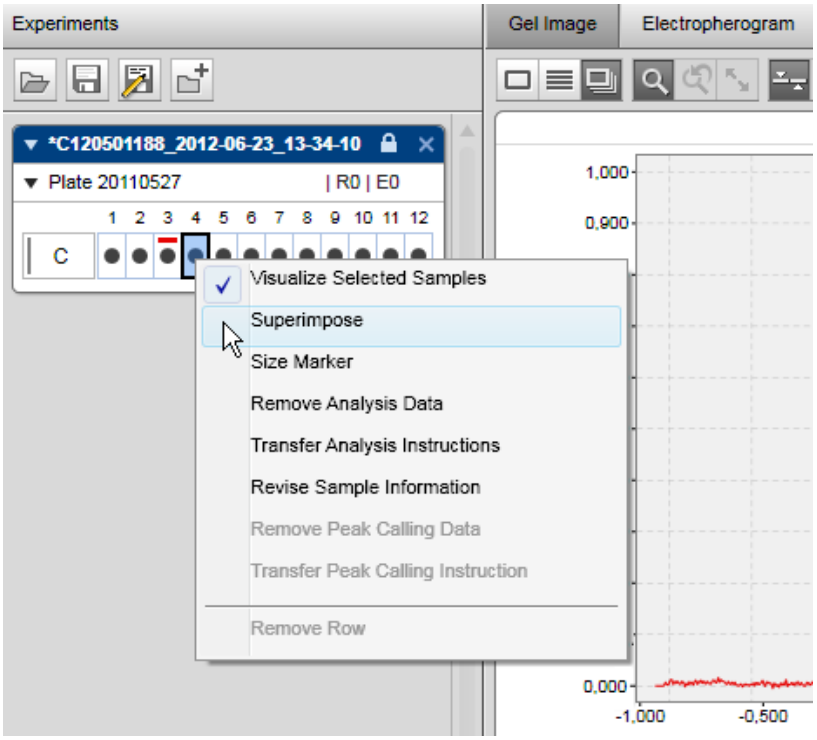
Activates vertical and horizontal rulers used to compare peak heights and positions.

Adding and removing samples

Unlike all other views, the superposition view does not automatically display all samples selected for visualization.

To add samples to the superposition view:

1. In the "Experiment Explorer" select the samples to be added.
2. Open the context menu of the selected samples in the "Experiment Explorer".
3. Select the "Superimpose" option.



Adding sample C4 to superposition.

The selected samples will be added to the superposition view. In the "Experiment Explorer" all samples that are displayed in the superposition view are marked by a colored rectangular according to their color in the superposition.

Note: Up to 12 electropherograms can be superimposed. A warning will be displayed if the limit is exceeded.

Alternatively, drag-and-drop up to 12 selected samples from the "Experiment explorer" to the superposition.

To remove samples from the superposition view, proceed as follows:

1. In the "Experiment Explorer" select the samples to be removed.
2. Open the context menu of the selected samples in the "Experiment Explorer".
3. Unselect the "Superimpose" option.

6.4.2.10 Inspecting sample properties

To view sample properties:

1. Select the sample in the "Experiment Explorer".
2. View the properties of the sample on the right-hand side of the analysis environment. If the toolbar on the right is not displayed, open it by clicking on the following icon:

In the properties view, there are five sections containing the following information:

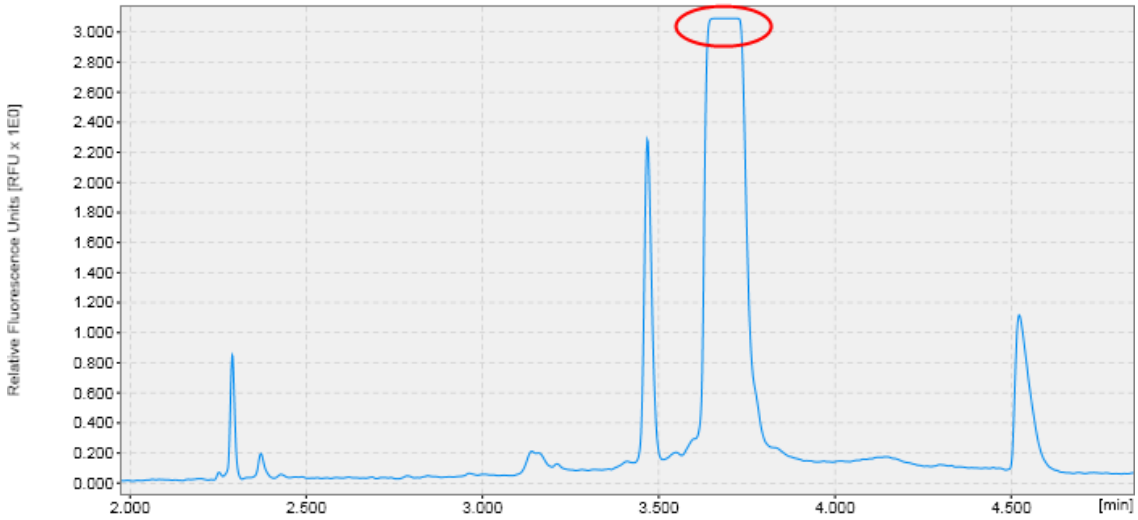
- Sample
  This section contains general information about the sample and the acquisition, for example, the date, experiment ID, and plate ID.
- Analysis instructions
  The analysis instructions section shows the analysis parameters, alignment marker, and the "reference marker" used for the analysis.
- Peak Calling Instruction
  This section shows the peak calling instruction that was last applied to the sample.
- Method
  This section shows the method name and actions used during the acquisition.
- Cartridge
  The cartridge section shows information about the cartridge, such as the cartridge ID and the cartridge type.
- Platform
  This section shows the software version and the instrument information (firmware version and serial number).

6.4.2.11 Saturated signals

Identifying a saturated signal

Overloading the signal by injecting highly concentrated DNA will cause the detector to saturate. Saturated signals are those in which the signal level exceeds the maximal detector limit.

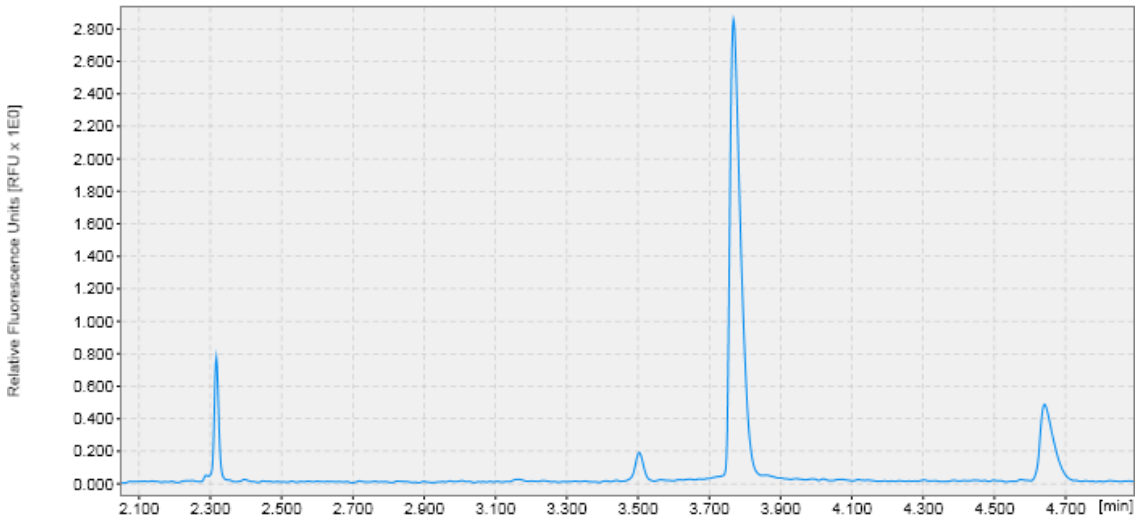
A saturated signal will usually display a flat top in its electropherogram. These signals are also referred to as “clipped”.



An example saturated signal.

Preventing a saturated signal

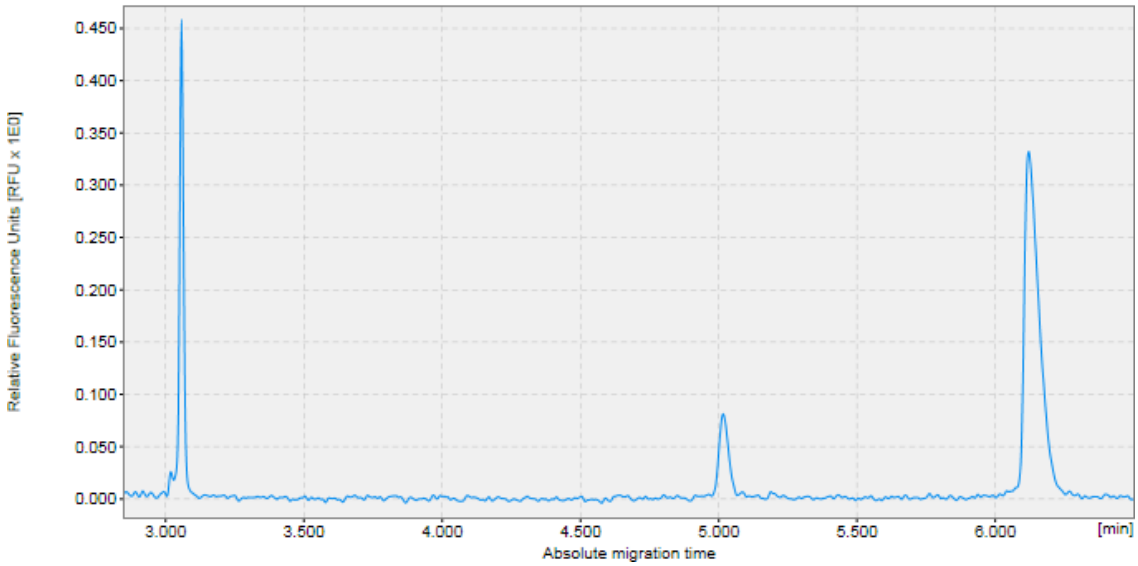
There are 2 ways to prevent overloading or saturation of the signal: dilute the samples in QX DNA Dilution Buffer or inject less sample. A smaller amount of sample can be injected by reducing the injection time (see section Operating the QIAxcel). A nonsaturated signal will display a sharp peak in the electropherogram.



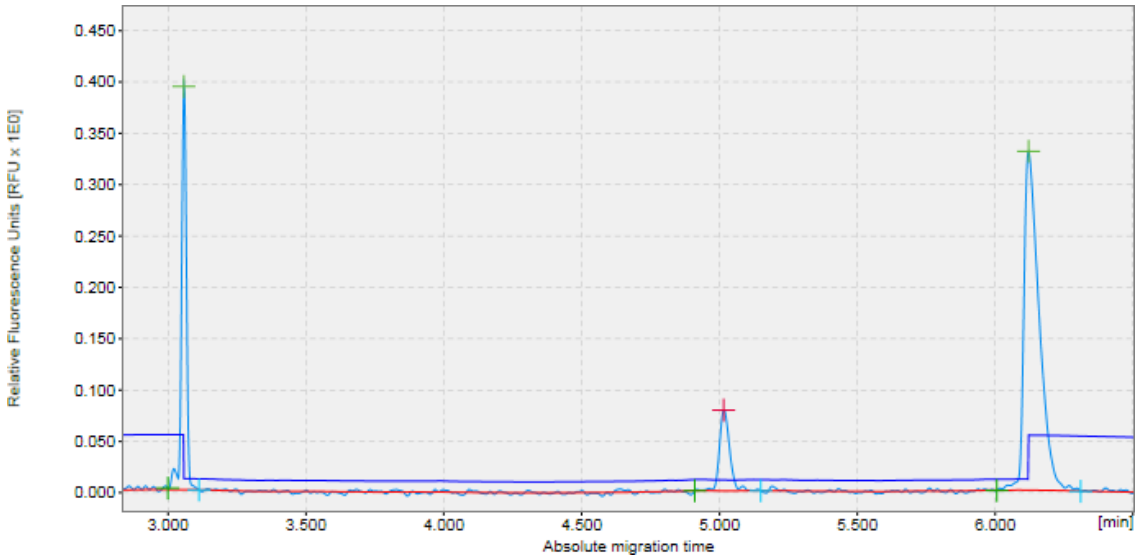
An example normal (nonsaturated) signal.

6.4.3 Peak detection

The analysis of samples is performed using a two-step approach. First, peaks are detected in the raw data. In a second step, the peak sizes and peak concentrations are determined by mapping the detected peaks to peaks of a "reference marker". This section describes the peak detection procedure. For size and concentration, see section Size and Concentration determination.



Unanalyzed raw data.



Raw data after peak detection, without determination of size and concentration.

Note: In the image above, the analysis parameter "Alignment Marker Threshold" (see dark blue line in the image above) was greater than the "Threshold" parameter. This leads to a peak in the threshold line at alignment marker positions.

6.4.3.1 Peak detection procedure

To perform peak detection, proceed as follows:

1. Load the samples you want to analyze using the "Experiment Explorer". For details, refer to the Loading sample data section.
2. Visualize the samples you want to analyze. See the Viewing sample data section for details on data inspection.
3. Select the samples for analysis.

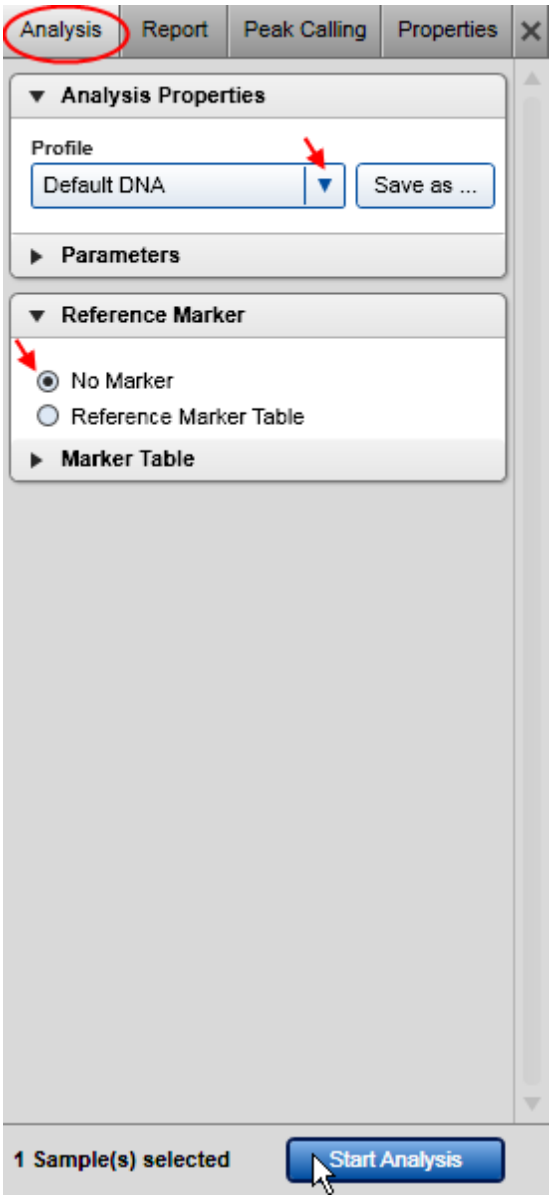
Note: Here, the selection inside the view is relevant — not the selection in the experiment explorer.
The way in which the samples can be selected depends on the view and on the number of samples to be selected:

View	Single sample selection	Multiple sample selection
Gel Image	Select a single sample by clicking the gel lane header of the sample. Selection of a sample for analysis in the "Experiment Explorer" is not possible in this environment.	Selection of multiple samples can be performed by clicking the gel lane headers using the "Shift" or "Ctrl" key (just as in the Windows explorer). Alternatively, you can select all visualized gel lanes by clicking the "Select all" key in the tool bar.
Single Electropherogram	Select a single sample in the "Experiment Explorer". In this view, the visualized sample will be analyzed.	Not possible in this view.
Electropherogram Overview	Select a single sample by clicking the electropherogram of the sample. Selection of a sample for analysis in the "Experiment Explorer" is not possible in this environment.	Selection of multiple samples can be performed by clicking the electropherograms using the "Shift" or "Ctrl" key (just as in the Windows explorer). Alternatively, you can select all visualized electropherograms by clicking the "Select all" key in the tool bar.
Electropherogram Superposition	Not possible in this view.	All samples included in the diagram are selected automatically.

4. Open the "Analysis" parameters panel to be able to specify the analysis properties.

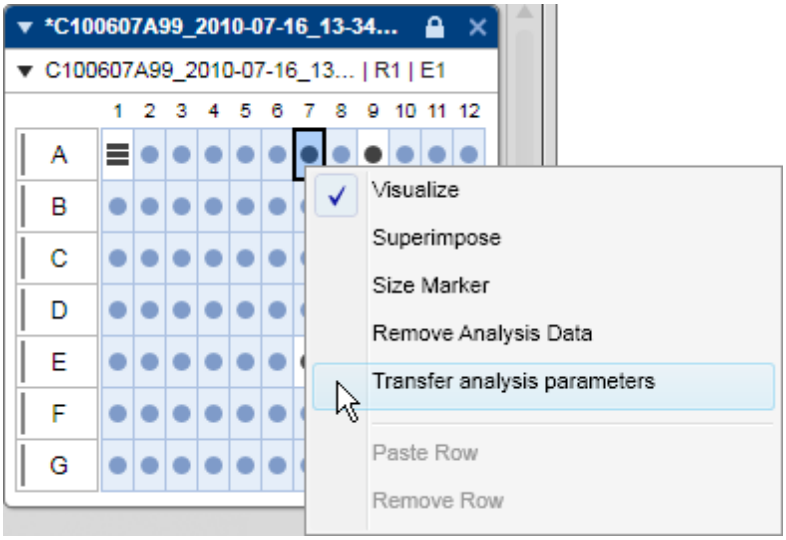
   If it is not visible, you can display it using the "View" menu (selecting the menu item "View"/"Show Analysis Parameters") or by clicking the icon at the extreme right of the view selection bar:

   In the "Analysis properties" panel, define the parameters to use for analysis. This can be done by selecting a predefined analysis profile, which can be either a default (e.g., "Default DNA") or a user defined parameter set. Alternatively, a new analysis profile can be created. To modify or create an analysis profile, refer to sections Modifying an analysis profile and Creating a new analysis profile, respectively. The analysis parameters of the selected profile are shown below the profile drop-down list. For general peak detection, no reference marker is required. Check "No Marker" in the "Reference Marker" section, as illustrated in the following figure.



No marker selected.

Note: If loaded samples have already been analyzed, the analysis parameters from the selected sample can be transferred to the "Analysis" parameters panel. To do this, select the menu item "Transfer analysis parameters" from the context menu in the "Experiment Explorer", as shown in the following figure.



Note: The alignment marker of a plate can be changed. To change the alignment marker, select the menu item "Overwrite alignment marker" from the context menu in the "Experiment Explorer" (the mouse cursor should be over the plate name). The "Overwrite Marker" dialog box appears. Select the alignment marker from the drop-down list and confirm your choice by clicking "OK".

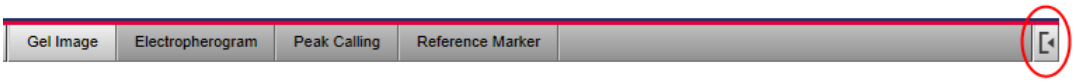
5. Start the analysis by clicking the "Start Analysis" button.
6. View the analysis results. For each analyzed sample, the results are shown in tabular form at the bottom of the "Analysis" environment in the "Peak Result" tab (see Result table section) and in the plot of the single electropherogram view (see Electropherogram view).
7. Save the analysis results by clicking the "Save" button in the "Experiment Explorer".

6.4.3.2 Modifying an analysis profile

To modify an analysis profile proceed as follows:

1. Open the "Analysis" tab at the right side of the "Analysis" environment.

   If it is not visible, you can display it using the "View" menu (selecting the menu item "View"/"Show Analysis Parameters") or by clicking the icon at the extreme right of the view selection bar:

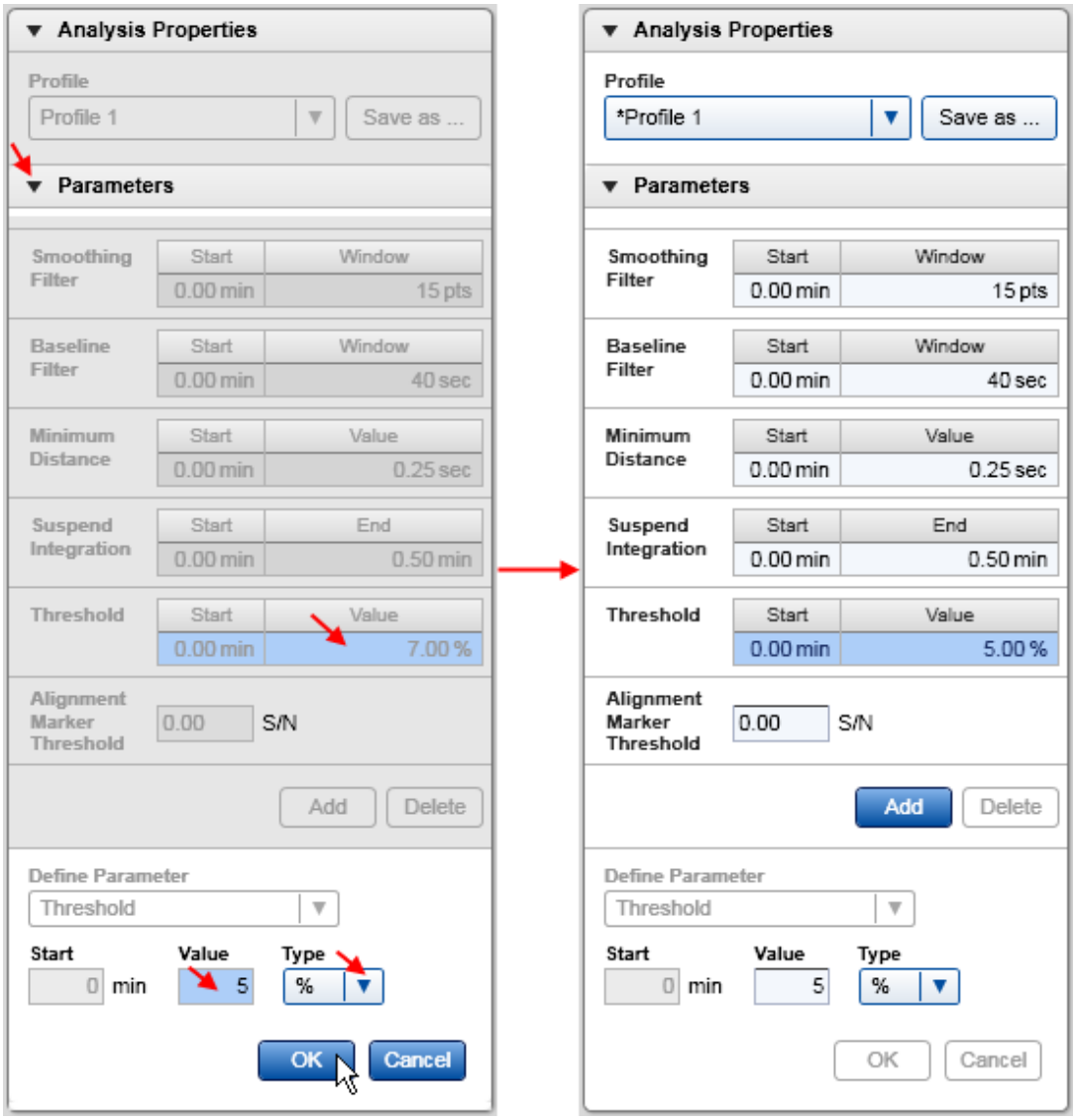


2. Select the analysis profile to be modified in the "Profile" drop-down list in the "Analysis Properties" panel .
3. Change the analysis parameters as described below.
4. To save the modified profile click the "Save as..." button to the right of the "Profile" drop-down list.

Note: The parameters of an analysis profile can be modified by users with assigned user role "Advanced User" only.

Parameters can be changed by:

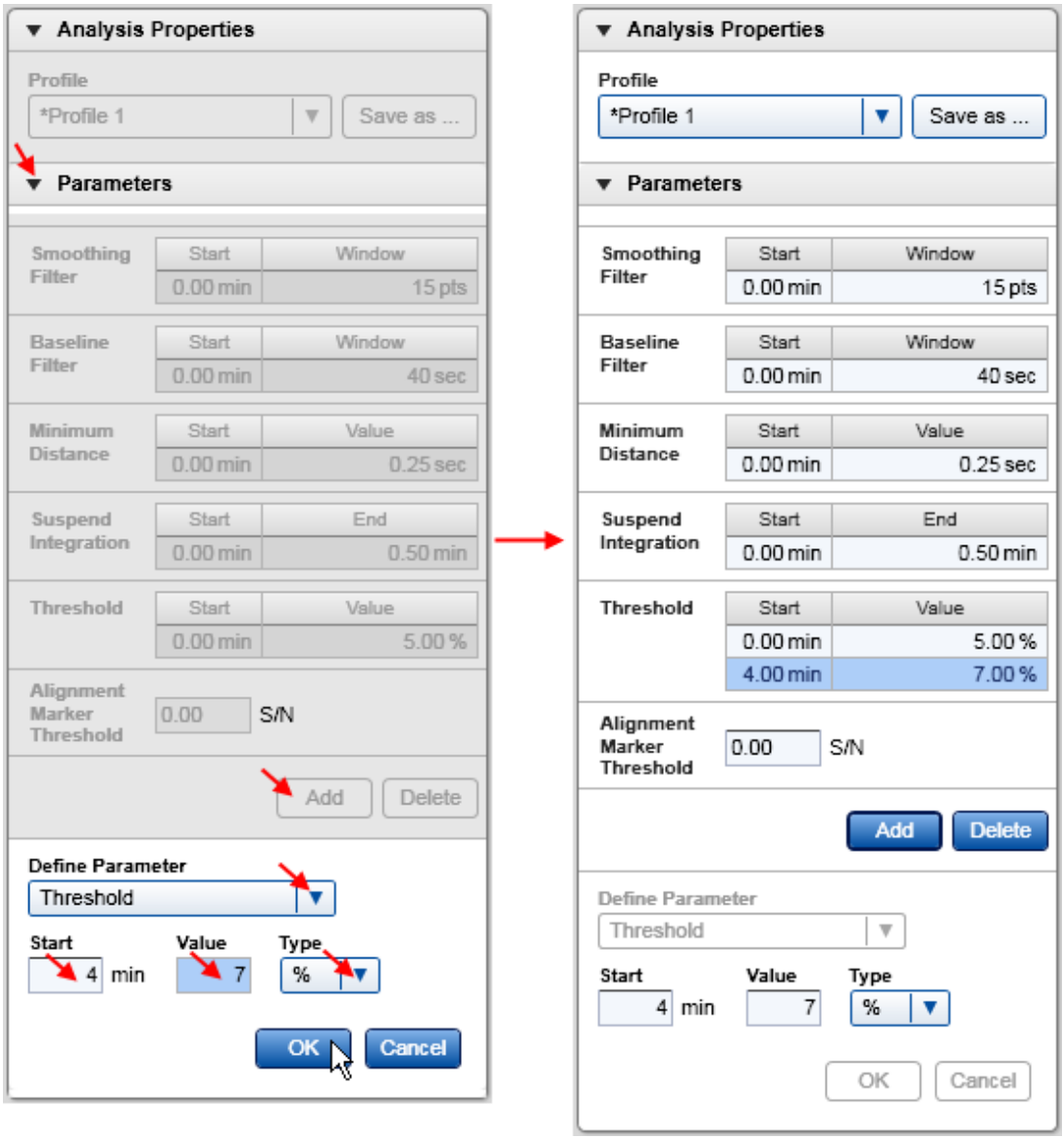
1. Clicking the parameter.
2. Changing the value (and unit if possible).
3. Clicking "OK".



Changing the threshold parameter.

For example, to raise the threshold parameter to 7% starting from 4 minutes, perform the following:

1. Click the "Add" button below the parameters.
2. Select the parameter type "Threshold".
3. Adjust the starting time (4 minutes), the threshold value (7), and its unit (%).
4. Accept the changes by clicking "OK".



Each parameter displayed in the figure above has a corresponding time point. This is necessary because all parameters, except for "Alignment Marker Threshold", can be changed with respect to time.

Note: The time of the initial parameter at 0.0 minutes cannot be changed. The suspend integration parameter is an exception. It is turned off by default and can be turned on to ignore a defined range of data during peak detection. This region does not necessarily start from 0.0 minutes.

The descriptions of the parameters and instructions on how to deduce suitable settings are in the table on the next page. More information about the analysis algorithms in QIAxcel ScreenGel and the respective parameters can be found in Appendix D.

Parameter	Description	Adjusting the value
Baseline Filter	This parameter governs the baseline detection (shown as a red line in electropherograms).	The default value for the "Window" parameter should be sufficient for most samples. If the baseline starts following the data, increase this value. Generally, the value should be set to twice the width of a single peak, but it must not be larger than half of the total migration time. If peak widths differ a lot over time, use distinct values for the "Window" parameter in different time intervals. For an example, see the "Default RNA" analysis parameter settings and Analyze RNA samples.
Threshold	The threshold parameter is used during peak detection. Signals that exceed the baseline by the threshold value are detected as peaks. The threshold can be given in RFU, as percentage of the highest signal in the sample, or as a multiple of the (estimated) noise level of the electropherogram.	The default setting is a good starting point for most samples. The threshold should be lowered if relevant peaks are below the threshold and not recognized as peaks. You can specify the threshold using different units. Use the "RFU" unit to set the threshold to a fixed RFU value. Use the "%" unit to specify the threshold as a percentage of the highest signal in the sample. Use the "S/N" unit to specify the threshold as a multiple of the noise level, which is estimated from the sample data. **Note**: The threshold parameter can be interactively changed in the "single electropherogram view". Simply drag the threshold (displayed in blue) with the mouse. When doing so, the sample is re-analyzed using the new threshold (all other parameters are taken from the sample properties).

Minimum Distance	The minimum distance parameter is used during the plausibility check of peaks. It defines the minimum distance two peak clusters must have to be detected as two distinct peaks. In noisy data with heavy tailing or fronting, noise spikes can cross the minimum peak threshold several times at the border of peaks. Detection of these noise peaks is prevented by this parameter.	The default setting is suitable for most samples. For very noisy data with fronting or tailing, in order to prevent the detection of noise peaks at cluster borders, increase the value.
Suspend Integration	The suspend integration parameter turns off peak detection for a defined period of time. The affected areas are marked with a grey bar in the single electropherogram view as well as in the electropherogram overview. Peaks that overlap with this bar are ignored by the analysis.	In the default setting, "Suspend Integration" is turned off, meaning that peak detection is performed on the entire duration of migration time. The time interval for "Suspend Integration" can be specified via absolute or relative migration time. In case the relative time unit is used, alignment marker peaks are not affected by "Suspend Integration". **Note:** The suspend integration interval is shaded gray in the electropherogram single view and overview.
Smoothing Filter	The smoothing filter parameter defines the smoothing window width, i.e., the strength of the smoothing. The smoothing filter improves the signal-to-noise ratio (S/N) of the data but lowers the resolution.	The default window width is a good setting for most samples. If two close peaks cannot be resolved, the smoothing filter parameter can be lowered or disabled (i.e., set to "0 pts") to obtain the optimal resolution. One example for disabled smoothing is the "Default Fast Analysis" profile.
Alignment Marker Threshold	This parameter allows to set a higher threshold for alignment marker peaks. It is useful to avoid that low intensity peaks are detected as alignment marker peaks, e.g. primer dimers before the lower alignment marker peak or noise peaks on the tail of the upper alignment marker.	A value between 5 and 10 should be suitable for most samples. If the alignment marker peaks have a lower S/N value, you can lower this threshold, or disable it by setting it to a value below the Threshold parameter.

6.4.3.3 Creating a new analysis profile

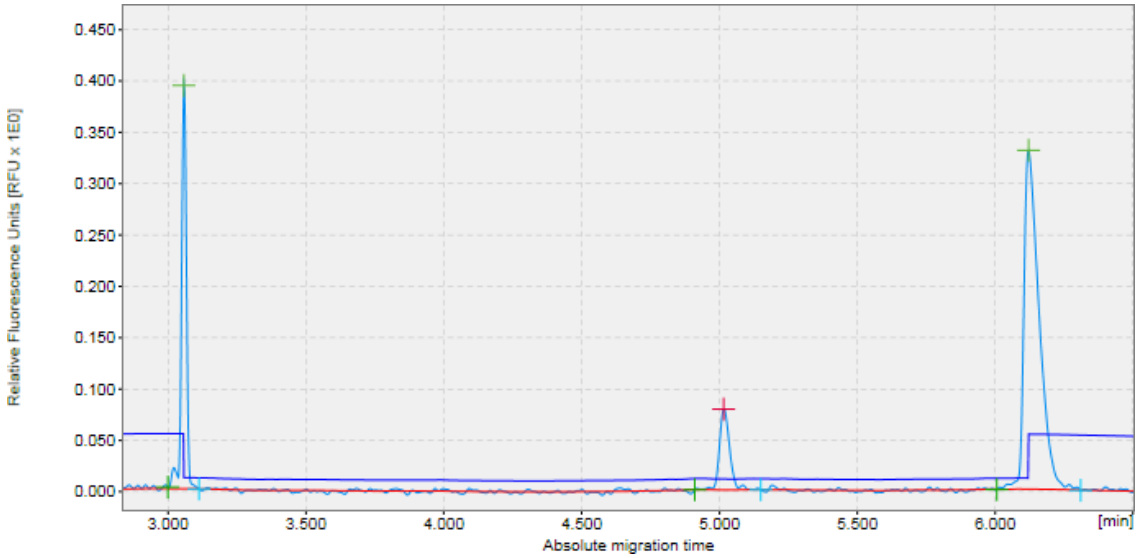
To create a new analysis profile:

1. Open the "Analysis" tab in the toolbar on the right-hand side of the "Analysis" environment.
2. Select an existing analysis profile from the "Profile" drop-down list. The selected profile serves as a template for the creation of the new profile. Select "NewAnalysisProfile" to start with default parameters.
3. Change the analysis parameters according your needs as described in the Modifying an analysis profile section.
4. Store the new profile by clicking the "Save as ..." button to the right of the "Profile" drop-down list.
5. Assign a unique name to the profile and click "OK".

Note: Only users with assigned user role "Advanced User" can create new analysis profiles.

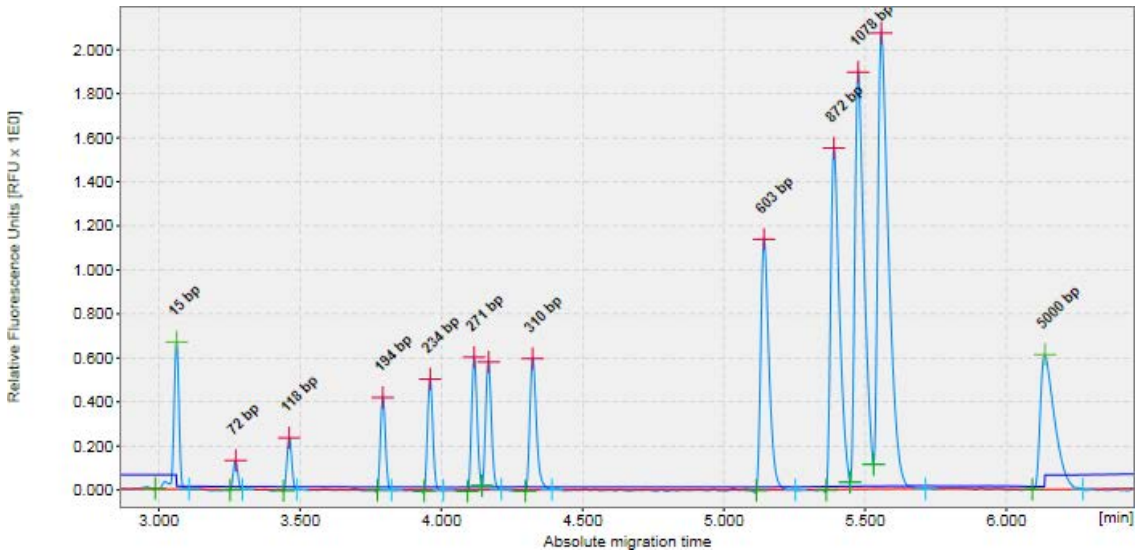
6.4.4 Size and concentration determination

For a sample with detected peaks, the sizes and concentrations of the underlying analytes are calculated by referencing to a sample containing fragments of known size and concentration. The figures below show how a so-called reference marker (middle picture) is used to derive the sizes and concentrations for detected peaks (upper and lower picture). A reference marker can be created in two ways: either a size marker sample is run side by side with the samples that are being analyzed or a previously saved reference marker is selected in the "Reference Marker" section in the analysis tab. For details, see Creating a reference marker.

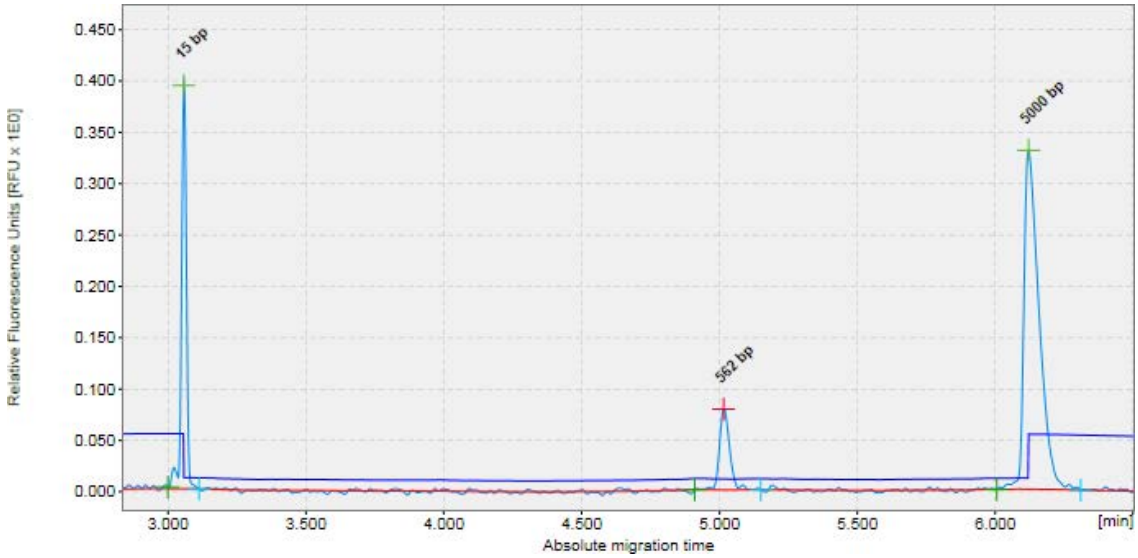


Sample with detected but not annotated peaks.

Each detected peak is mapped to a corresponding reference marker peak. For peaks without unique corresponding reference marker peaks, the adjacent reference marker peaks are taken as reference (e.g., peaks with known size 310 bp and 603 bp, respectively).



Reference marker sample. Sizes and concentrations of contained molecules are known.



Sample with detected and annotated peaks.

The sizes for the newly detected peaks are either directly transferred from the matching reference marker peaks (15 bp peak) or interpolated using the two adjacent reference marker peaks (562 bp peak interpolated from 310 bp and 603 bp).

Similarly, the concentrations of detected analytes are referred from the known concentrations underlying the corresponding reference marker peaks.

This section describes how to proceed to determine size and concentration.

Note: Sample analysis can be performed by users with the assigned user roles "Basic User" and "Advanced User" only.

6.4.4.1 Size and concentration determination procedure

To determine size and concentration, proceed as follows:

1. Load the samples you want to analyze using the "Experiment Explorer". For details refer to the Loading sample data section.
2. If a size marker was run side by side with samples, create a new reference marker as described in Creating a reference marker.
3. Perform steps 2 to 4 of the peak detection procedure described in Peak detection procedure.

   After selecting the analysis profile, in the "Reference Marker" section, check "Reference Marker Table" and select a previously saved reference marker. Details of the "reference marker" are shown below the combo-box.

Reference marker checked.

Note: If you just created a new reference marker in step 2, it is preselected for use. Proceed with step 4.

Note: To ensure compatibility, the reference marker drop-down list contains only reference marker tables that match the alignment marker of the selected samples. The drop-down list is marked as invalid and empty if there is no matching reference marker table. In this case, check the sample alignment marker and correct it if required (refer to Checking alignment marker), or create a new reference marker (refer to Creating a reference marker).

Note: If no sample is selected, the reference marker drop-down list is empty. Select the samples to analyze before selecting the reference marker. For details see Selecting samples for analysis or report.

Note: See the table below for explanation of the symbol at the right of the "Reference Marker Table" drop-down list:

●	The selected reference marker table is **fully compatible**. That means that the size marker used for the reference marker table was processed no earlier or later than 90 days (DNA)/60 days (RNA, protein) as the sample, and with the same cartridge and method as the sample. For analysis, it is not necessary to run the size marker first. The user can analyze older samples with a newer reference marker as well.
●	The size marker used for the reference marker table was processed **more than 90 days** (DNA)/**60 days** (RNA, protein) earlier or later than the sample, with the same cartridge and method as the sample.
●	The reference marker table was processed with the same method as the sample, but with **another cartridge** of the same cartridge type.
●	The reference marker table is **not compatible** with the sample. This can happen if no reference marker matches the cartridge type, method and alignment marker of the sample.

Important: Selecting the correct size marker will increase the accuracy of the size and concentration determination. Use the marker containing DNA fragments closest to the size of your targeted DNA fragments. The DNA fragments to be analyzed must fall within the smallest and largest fragment size of the size marker. In addition, the range of the alignment marker must cover the range of the size marker.

4. In order to start the analysis and view and save the results, perform steps 5 to 7 as described in the section Peak detection procedure.

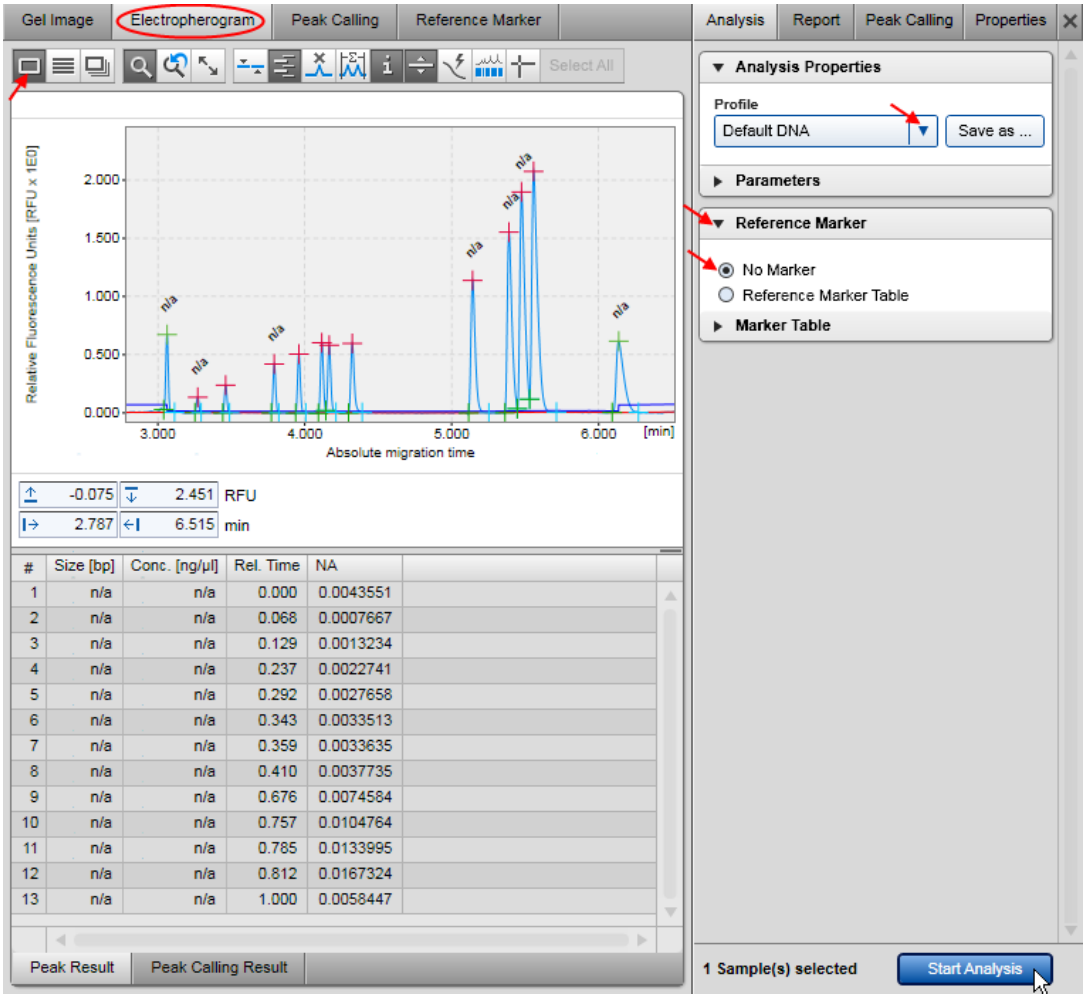
Note: It is possible to reuse the analysis parameters and the reference marker table of an analyzed sample. Right-click the sample in the experiment explorer and select the context menu option "Transfer Analysis Instruction". The analysis parameters and the reference marker table, if present, from the sample will be transferred to the analysis parameters tab.

6.4.4.2 Creating a reference marker

To create a new reference marker, an analyzed size marker sample with annotated peak times and areas is required. A reference marker is formed by matching the peaks of the size marker sample to a size marker table (including alignment marker).

Proceed as follows:

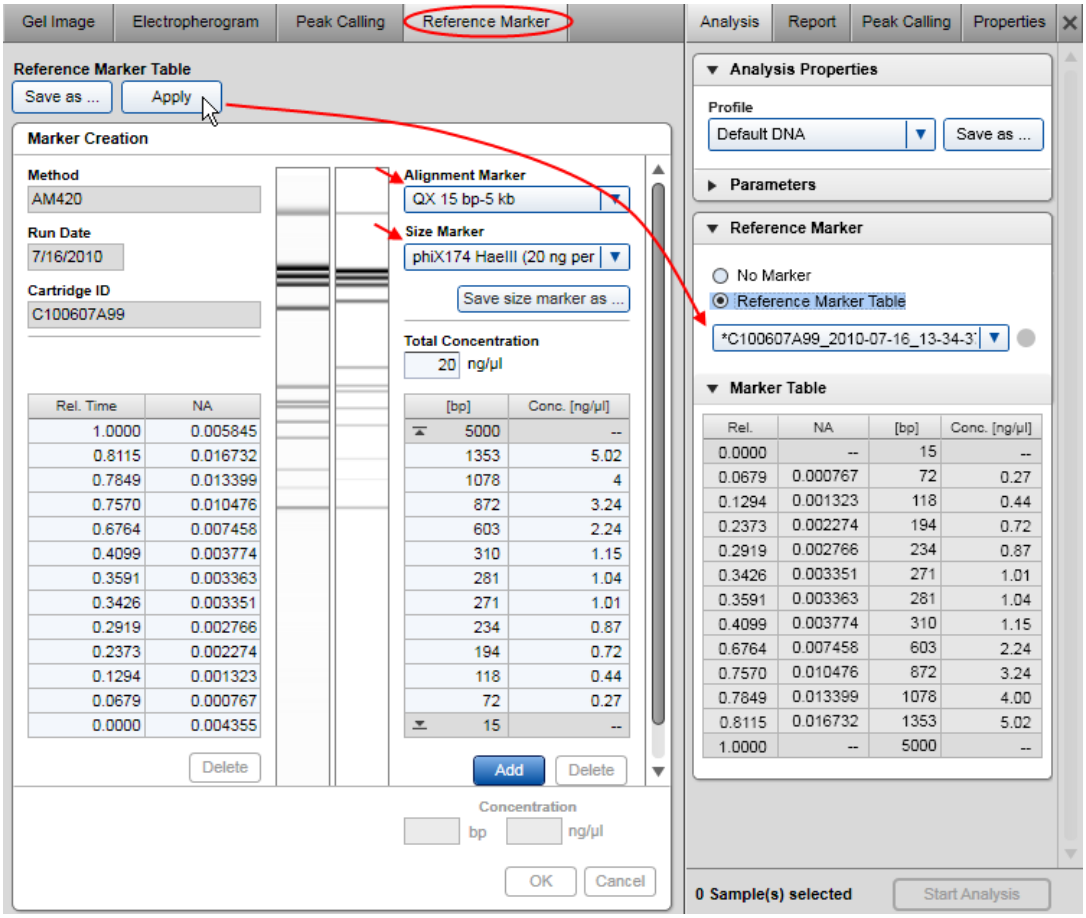
1. In the "Experiment Explorer" select the sample that contains the size marker. If it is not flagged as "Size Marker" (i.e., its symbol is or), flag it with a right-mouse click and by selecting the "Size Marker" option from the context menu that appears. The icon changes to or .



Analyzing the size marker sample.

2. Open the size marker sample in "single electropherogram view".
3. Select a profile in the "Analysis Properties" toolbar or use the default parameters of "NewAnalysisProfile".
4. Select "No Marker" as reference marker
5. Start the analysis.
   The result of the analysis is a sample with annotated peak times and areas.
6. Make sure that the right peaks were detected. Use the "Insert/Delete Peak" options described in the Manually modifying analysis results section or change the analysis parameters and reanalyze the size marker sample.
7. Switch to the "Reference Marker" screen.
   The peak table (with the "Rel. Time" and "NA" columns) of the size marker sample is displayed at the left side of the screen.

   Note: The panel is empty if no size marker samples are selected in the "Experiment Explorer" or if the selected size marker sample is not analyzed. In this case, repeat the steps above first.



Creating the reference marker.

Note: Depending on cartridge and method, a size marker creates different gel lanes. As the gel lane for the size marker (right-hand side) is a calculation based on the size marker table only, this image may differ from the gel lane from the actual run (left-hand side).

8. In the "Reference Marker" screen select the alignment marker and size marker used in the size marker sample.
   A comparison of the sample gel view (left) and the theoretical reference marker gel view (right) is displayed in the middle of the screen.

   Note: Creating new size markers is described in Creating a new size marker table.

9. If the number of peaks in the size marker sample matches the number of peaks in the reference marker (two alignment marker peaks plus the size marker peaks), the reference marker can be used for sample analysis. Click the "Apply" button at the top of the "Reference Marker" screen to copy the created reference marker to the bottom of the "Reference Marker" panel of the "Analysis" parameters screen.

   Optionally, save the reference marker using the "Save as..." button at the top of the screen if you want to use the reference marker table for the analysis of further experiments.

   Note: The "Apply" and "Save as..." buttons are disabled and a warning is displayed at the top of the screen if the reference marker is invalid, e.g., if the number of peaks on the left and on the right does not match.
   If more peaks than expected were detected in the size marker sample, you can delete them using the "Delete" button below the size marker samples peak table (with "Rel. Time" and "NA").

Alternatively, switch to the single electropherogram view and check that the correct peaks were detected. Use the "Insert/Delete Peak" options described in the Manually modifying analysis results section or change the analysis parameters and reanalyze the size marker sample.

Note: A reference marker can be created by users with the assigned user role "Basic User" and "Advanced User" only.

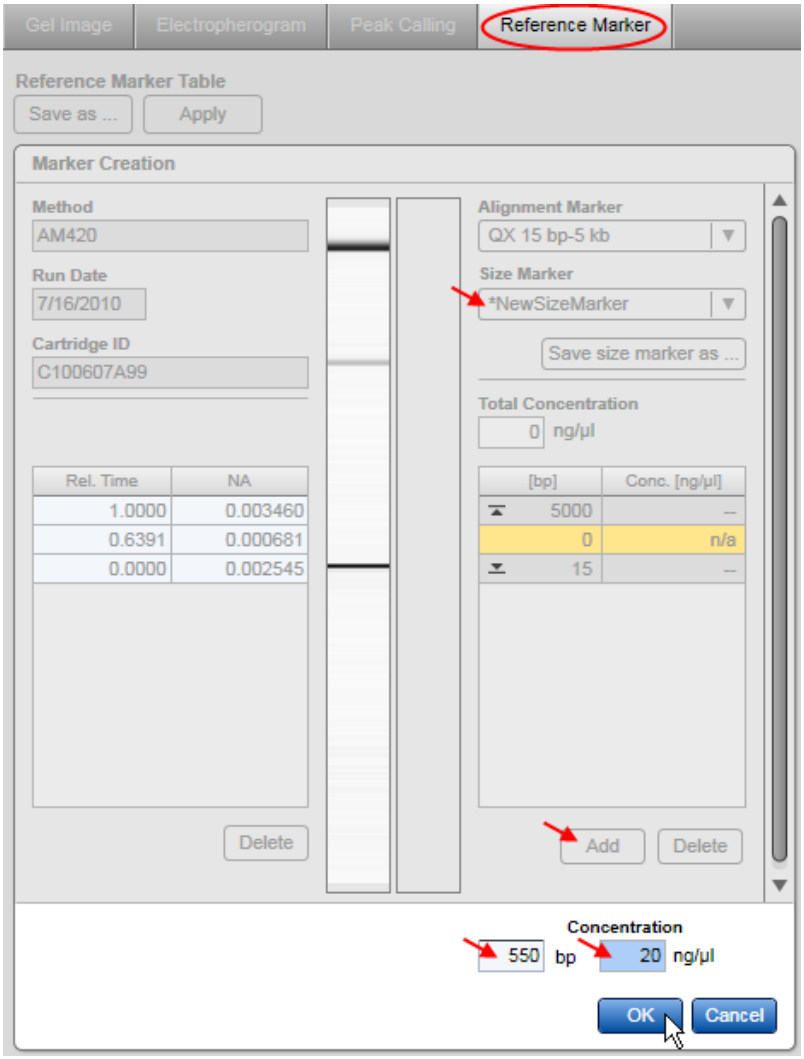
To continue sample analysis refer to step 3 of the Size and Concentration determination procedure

6.4.4.3 Creating a new size marker table

To use a custom size marker, a new size marker table has to be created manually.

Proceed as follows:

1. In the "Experiment Explorer" select the sample that contains the size marker. If it is not flagged as "Size Marker" (i.e., its symbol is or), flag it with a right-mouse click and by selecting the "Size Marker" option from the context menu that appears. The icon changes to or .
2. Open the "Reference Marker" screen of the "Analysis" environment.



Editing a new size marker.

3. Select "NewSizeMarker" from the size marker drop-down list to create an empty size marker table.
4. Click the "Add" button below the table to add a new row to the table.
5. Define the size and optionally the concentration.
6. Click "OK" to save the changes to the table. Repeat the steps from step 4 to define all rows.
7. Save the new size marker by clicking the "Save Size Marker as..." button below the size marker drop-down list.

Note: A new size marker can be created by users with the assigned user role "Advanced User" only.

Note: In protein mode, no concentration values can be edited.

Note: If a sample is selected which is flagged as a size marker, a warning about mismatch of the number of rows of the size marker and peak table of the selected sample may be displayed as shown in the figure above.

6.4.5 Peak Calling

Based on the peak table, which is the result of the sample analysis, a peak calling step can be performed.

Peak calling shows whether corresponding peaks (e.g., because of the same size) are present in analyzed samples, and provides peak data for comparison.

To trigger peak calling, the definition of the peaks of interest must be provided by the user. Refer to the Creating a new peak calling instruction section for information about how to create it.

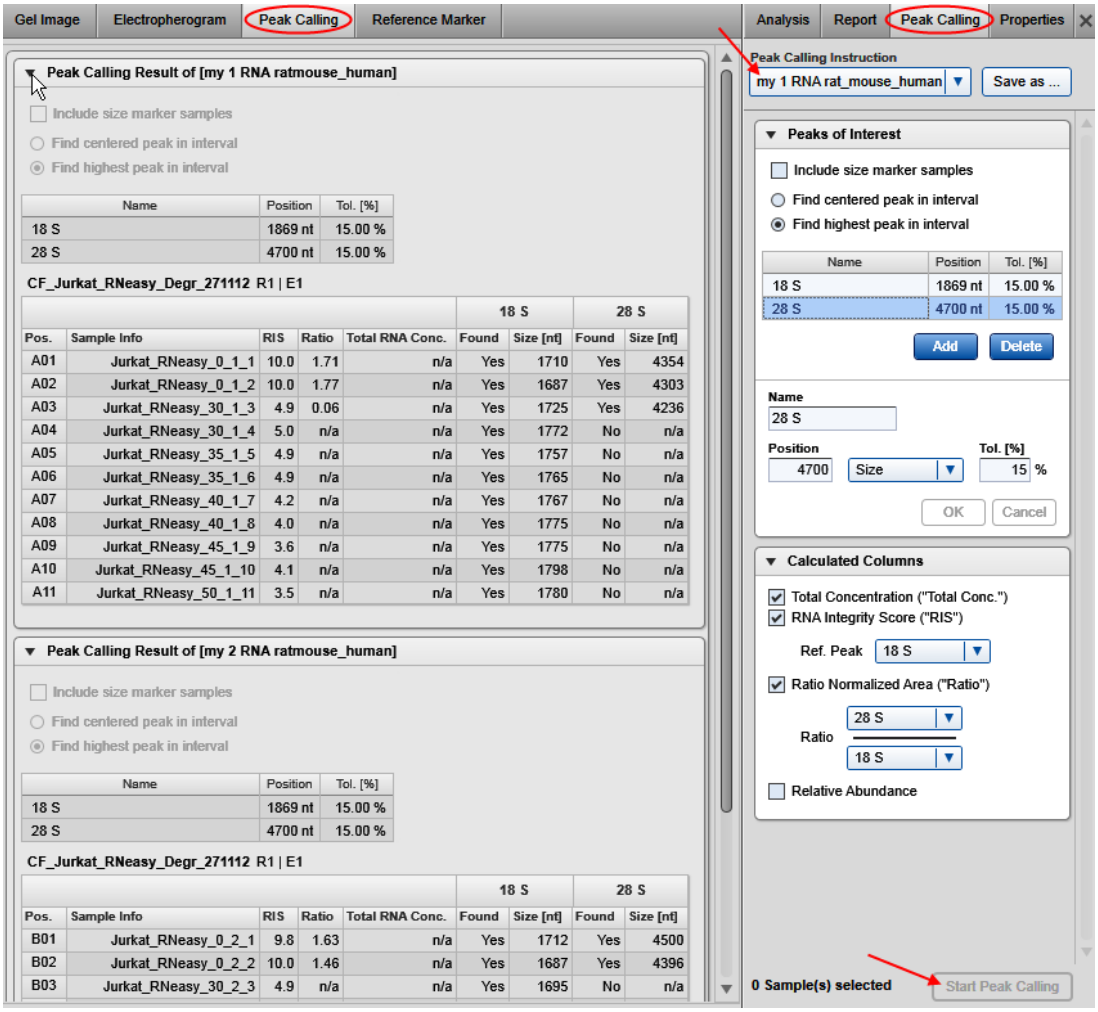
Note: Peak calling can be performed by users with the assigned user roles "Basic User" and "Advanced User" only.

To perform peak calling proceed as follows:

1. Load and activate the experiment for which sample peak calling should be carried out.
2. Analyze the samples of interest as described in Analysis procedure if not yet analyzed.

   Note: The samples must be analyzed before performing peak calling.
3. Select the visualized samples that the peak calling instruction shall be applied to.
4. Open the "Peak Calling" tab located on the right-hand side of the "Analysis" environment.
5. Select the peak calling instruction from the "Peak Calling Instruction" drop-down box, which contains the set of peaks to search for.
6. Start peak calling by clicking the "Start Peak Calling" button at the bottom of the "Peak Calling" tab. The peak calling instruction is assigned to the selected samples and the "Peak Calling" screen in the middle of the "Analysis" environment is filled with the peak calling result.

   Note: If you click "Start Peak Calling" the next time with the same unchanged peak calling instruction, the previous peak calling result for this instruction is completely replaced by the new one. If you would like to apply the same peak calling instruction to different data and don't want to overwrite the first set of results, save the instructions under different names, and apply them subsequently to the different sets of samples.
7. Switch to the "Peak Calling" screen in the middle of the "Analysis" environment to view the result. The structure of the result is described below.


Gel Image
Electropherogram
Peak Calling
Reference Marker
Analysis
Report
Peak Calling
Properties
Peak Calling Result of [my 1 RNA ratmouse_human]
Include size marker samples
Find centered peak in interval
Find highest peak in interval
Name Position Tol. [%]
18 S 1869 nt 15.00 %
28 S 4700 nt 15.00 %
CF_Jurkat_RNeasy_Degr_271112 R1 | E1
Pos. Sample Info RIS Ratio Total RNA Conc. 18 S Found 18 S Size [nt] 28 S Found 28 S Size [nt]
A01 Jurkat_RNeasy_0_1_1 10.0 1.71 n/a Yes 1710 Yes 4354
A02 Jurkat_RNeasy_0_1_2 10.0 1.77 n/a Yes 1687 Yes 4303
A03 Jurkat_RNeasy_30_1_3 4.9 0.06 n/a Yes 1725 Yes 4236
A04 Jurkat_RNeasy_30_1_4 5.0 n/a n/a Yes 1772 No n/a
A05 Jurkat_RNeasy_35_1_5 4.9 n/a n/a Yes 1757 No n/a
A06 Jurkat_RNeasy_35_1_6 4.9 n/a n/a Yes 1765 No n/a
A07 Jurkat_RNeasy_40_1_7 4.2 n/a n/a Yes 1767 No n/a
A08 Jurkat_RNeasy_40_1_8 4.0 n/a n/a Yes 1775 No n/a
A09 Jurkat_RNeasy_45_1_9 3.6 n/a n/a Yes 1775 No n/a
A10 Jurkat_RNeasy_45_1_10 4.1 n/a n/a Yes 1798 No n/a
A11 Jurkat_RNeasy_50_1_11 3.5 n/a n/a Yes 1780 No n/a
Peak Calling Result of [my 2 RNA ratmouse_human]
Include size marker samples
Find centered peak in interval
Find highest peak in interval
Name Position Tol. [%]
18 S 1869 nt 15.00 %
28 S 4700 nt 15.00 %
CF_Jurkat_RNeasy_Degr_271112 R1 | E1
Pos. Sample Info RIS Ratio Total RNA Conc. 18 S Found 18 S Size [nt] 28 S Found 28 S Size [nt]
B01 Jurkat_RNeasy_0_2_1 9.8 1.63 n/a Yes 1712 Yes 4500
B02 Jurkat_RNeasy_0_2_2 10.0 1.46 n/a Yes 1687 Yes 4396
B03 Jurkat_RNeasy_30_2_3 4.9 n/a n/a Yes 1695 No n/a
Peak Calling Instruction
my 1 RNA rat_mouse_human
Save as ...
Peaks of Interest
Include size marker samples
Find centered peak in interval
Find highest peak in interval
Name Position Tol. [%]
18 S 1869 nt 15.00 %
28 S 4700 nt 15.00 %
Add
Delete
Name
28 S
Position
4700
Size
Tol. [%]
15 %
OK
Cancel
Calculated Columns
Total Concentration ("Total Conc.")
RNA Integrity Score ("RIS")
Ref. Peak
18 S
Ratio Normalized Area ("Ratio")
28 S
Ratio
18 S
Relative Abundance
0 Sample(s) selected
Start Peak Calling

Separate RNA analysis for row A and B with RNA peak calling.

8. To save the result of peak calling, save the experiment by clicking the "Save" button in the "Experiment Explorer".

Peak calling result

Every sample can be analyzed individually (by means of peak calling). Therefore, the peak calling result overview is grouped by peak calling instructions, each of them named as the applied peak calling instruction (see image above). The result for each peak calling instruction can be collapsed individually. It has the following structure: the table with the peak calling instruction is placed at the top, followed by the list of the samples to which the peak calling instruction has been applied. The list of the samples is grouped by the plates to which the samples belong.

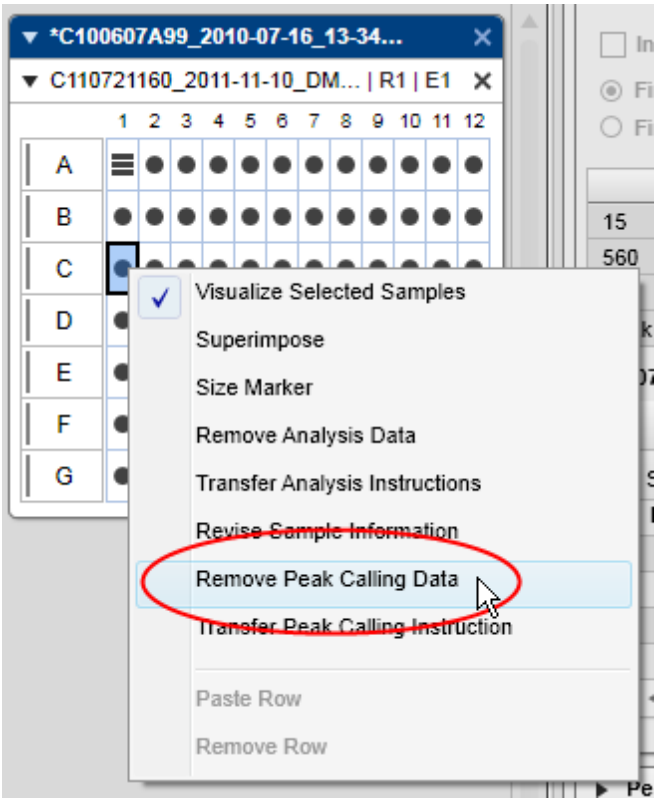
Each row in the table corresponds to a sample; the columns "Pos." and "Sample Info" identify the sample. The "Pos" column is fixed. The following columns are defined by the peak calling instruction. Aggregated columns over all peaks of interest appear if they were selected in the "Calculated Columns" panel of the peak calling instruction. The following columns are grouped by the names of the peaks of interest and show several peak properties. To change the properties listed for each peak of interest, right-click the table header and select/unselect the property with the "Show Column" option. The change takes effect in the entire peak calling result overview.

Note: If a sample was not analyzed, it is not present in the peak calling result overview.

Parts of the peak calling result table can be copied to the clipboard. Select the cells to be copied and then press "Ctrl" + "C". To copy the complete result of a peak calling instruction, right-click in the peak calling result table and select the "Copy Peak Calling Result of [...]" option.

Removing peak calling result

To remove the result of peak calling from a sample, right-click the sample in the experiment explorer and select "Remove Peak Calling Data" from the context menu that appears, as shown in the figure below. This menu item is only active if peak calling has been performed for the sample.



Remove the result of peak calling from a sample.

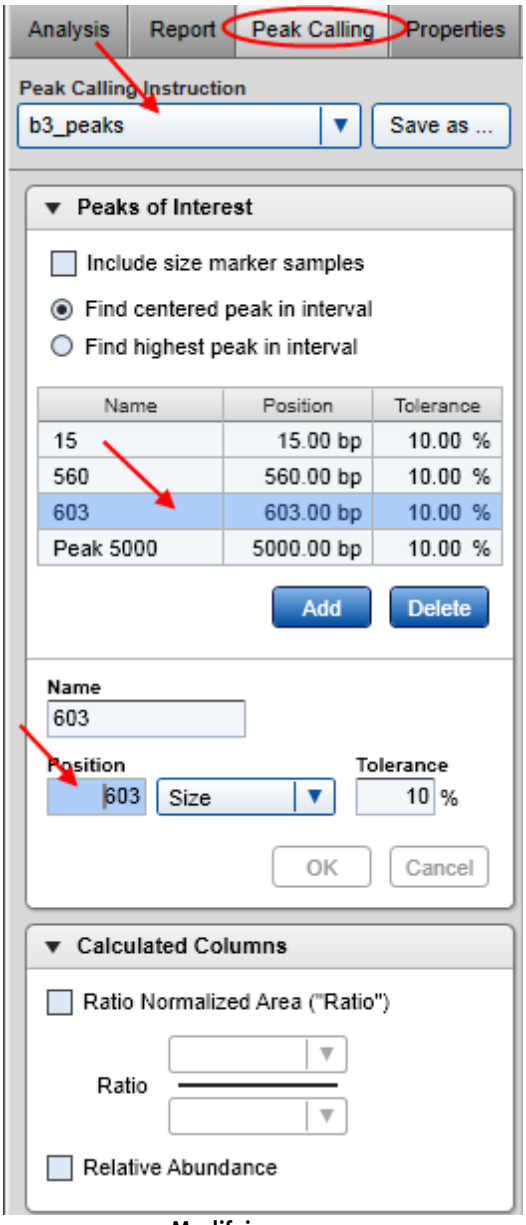
6.4.5.1 Modifying a peak calling instruction

Peak calling instructions contain a set of parameters, defining the peaks to search for (peaks of interest).

Note: Peak calling instructions can be modified by users with the assigned user role "Advanced User" only.

To modify a peak calling instruction proceed as follows:

1. Open the "Peak Calling" tab at the right of the "Analysis" environment.
2. Select the peak calling instruction to be modified from the "Peak Calling Instruction" drop-down box.
3. Change the definitions for the peaks of interest according to your needs as described below.



Modifying a row.

Note: The name in the "Peak Calling Instruction" drop-down box will appear with an asterisk to the left, indicating that the table has been changed.

4. Save the modified peak calling instruction by clicking the "Save as..." button to the right of the "Peak Calling Instruction" drop-down box.

Peak calling configuration:

Include size marker samples	If this option is chosen, peak calling can be performed on the size marker sample too. Otherwise, peak calling will be skipped for size marker samples.
Find centered / highest peak in interval	If more than one peak is found within the tolerance interval, this setting determines whether the centered peak (nearest to the sought position) or the highest peak is chosen.

To add a peak of interest:

1. Click the "Add" button. A new row with empty fields will appear at the bottom of the table.
2. Specify the peak of interest in the edit area below.

Name	Specifies the name of the peak of interest. This will be the column header in the peak calling result table. **Note**: The names of the peaks must be different.
Position	Specifies the position of the peak to search for and the unit of the position (Size/ Molecular Mass, Rel. Time, or Time). **Note**: The positions of the peaks must be different.
Tolerance	Tolerance for peak searching. In a sample the peak will be considered as detected if its position difference is less than the given tolerance from the defined position.

Optionally, in protein mode, there are additional fields provided to specify a reference protein for absolute quantification:

Reference Position	The plate position of the reference protein with known concentration. **Note**: The reference protein must been separated side by side with samples.
Concentration	The known concentration of the reference protein.

3. Click "OK" to add the new peak of interest to the table.

   Note: The peaks of interest are sorted by position in the peak calling instruction table.

To delete a peak of interest:

1. Select the peaks row in the table.
2. Click the "Delete" button.

To modify a peak of interest:

1. Select the row of the peak of interest to be modified.

2. Edit the values of the peak of interest in the edit area below.
3. Click "OK". The values in the selected row are changed.

   Note: The peaks of interest are sorted by position in the peak calling instruction table.

Calculated columns:

In addition to finding the specified peaks, depending on the run mode, the following parameters can be calculated during peak calling:

Total Concentration	For RNA mode only. The total concentration of the RNA over the whole sample.
RNA Integrity Score	For RNA mode only. RNA integrity score (RIS) is a value from 0 to 10, where a value of 10 indicates completely intact RNA. This is especially useful for RNA QC. **Note:** The value is not calculated if the 18S peak was not found.
Ratio Normalized Area	For DNA and RNA mode only. Choose two peaks of interest. If both are found in the sample, the ratio of their normalized areas is calculated. This is especially useful for RNA QC using the 28S and 18S peaks.
Relative Abundance	For each peak of interest, the normalized area relative to the highest normalized area of corresponding peaks over all samples is calculated. (For the sample in which the normalized area of the peak is highest, the relative abundance is 100%. For all other samples, it is the percental fraction of its normalized area relative to the highest value.)
Absolute Concentration	For protein mode only. For each peak of interest with a given reference protein, the concentration is calculated based on the normalized area of the reference protein peak analyzed side by side with the sample. **Note**: The value is not calculated if the peak of interest is not found in the sample or the reference. In this case, "n/a" is displayed. The value is also not calculated if the reference is not part of the peak calling overview result table.

6.4.5.2 Creating a new peak calling instruction

To create a new peak calling instruction:

1. Open the "Peak Calling" tab at the right of the "Analysis" environment.
2. Select a peak calling instruction from the "Peak Calling Instruction" drop-down box. The selected peak calling instruction serves as a template for the creation of the new one. Select "NewPeakCallingInstruction" to start with an empty table.
3. Specify the peaks of interest according to your needs as described in the Modifying a peak definition table section.
4. Save the new peak calling instruction by clicking the "Save as..." button to the right of the "Peak Calling Instruction" drop-down box. Enter a new unique peak calling instruction name and click "OK".

6.4.6 Analysis of DNA samples

This section describes how to analyze a DNA sample. It distinguishes between two types of analysis: (1) standard analysis of DNA samples; (2) analysis of samples that were run using the high voltage method (fast analysis). For both types of samples, perform steps 1–6. Then, switch to the subsection referring to the type of analysis required by your samples.

1. Switch to DNA mode if this is not already selected. For details, refer to section Modes.
2. Load the samples you want to analyze using the "Experiment Explorer". For details, refer to the Loading sample data section.
3. If a size marker was run side by side with samples, create a new reference marker as described in Creating a reference marker.
4. Visualize the samples you want to analyze. See the Viewing sample data section for details on data inspection.
5. Select the samples to be analyzed. See the Selecting samples for analysis or report section for details.
6. Open the "Analysis" parameters panel to be able to specify the analysis properties.

Continue with the standard analysis of DNA samples (see below), or with the analysis of "Fast Analysis" samples (see below).

Standard analysis of DNA samples

1. Select the "Default DNA" analysis profile.

   Note: The QIAxcel ScreenGel software version 1.2. comes with an improved default profile, named "Default DNA v2.0". To be independent from the highest signal in the sample, in the new profile, the threshold parameter is defined as a multiple of the noise level, which is estimated from the sample data.

2. In the reference marker section, check "Reference Marker Table" and select a previously saved reference marker.
3. Click the "Start Analysis" button to start the analysis.

   Ensure that the peak detection has worked as expected. The single electropherogram view is most suitable for checking peak detection.

   If the raw data being analyzed are too noisy, increase the smoothing filter window. Click this parameter line and set the window size to 25 pts, for example. To apply time-dependent smoothing, add one or more smoothing filter parameter lines. To do so, click the "Add" button, select "Smoothing Filter", and set the values for start time and window size. Click "OK" to confirm this setting. An example of time-dependent smoothing is represented by the "Default RNA" analysis profile in RNA mode.

   If peaks were detected before or after the alignment marker peak, increase the alignment marker threshold.

   If in a certain range of migration time, peak detection is too sensitive, increase the threshold in this region. In the "Analysis Properties" section, click the "Add" button and select "Threshold" from the parameters drop-down list. As a starting point, set the time where the region for which to increase the threshold starts, and define a threshold of, for example 5 S/N. Click the "OK" button to confirm this setting. Then, at the end of the affected region, reset the threshold to the default value (e.g., 2 S/N in "Default DNA") by adding a third threshold definition. Set the start time of this threshold to the end of the affected region and set the threshold value to that of the first threshold parameter line. Click the "OK" button to confirm this setting.

   Click the "Start Analysis" button again to start a new analysis according to this modified analysis profile.

   In some cases, it may be necessary to repeat the adaptations to the analysis profile iteratively. If the peak detection worked as expected with the modified analysis profile, save this analysis profile and try to use this new profile instead of the "Default DNA" analysis profile for future DNA analyses of similar samples.

   Note: For detailed information on how to modify parameters of an analysis profile, refer to section Modifying an analysis profile.

   Note: Only users with user role "Advanced User" can modify and save parameters of an analysis profile. Users with user role "Basic User" can select another analysis profile which is more suitable for the type of samples.

"Fast analysis" of DNA samples

1. Select the "Default Fast Analysis" analysis profile.
2. In the reference marker section, check "Reference Marker Table" and select a previously saved reference marker.
3. Click the "Start Analysis" button to start the analysis.

Note: When analyzing "Fast Analysis" data, it may be that the default baseline filter window (40 seconds) is too large. In this case, a notification will arise suggesting to decrease the baseline filter window. To do so, click the baseline filter parameter and set the window size to 39. In most cases, this will work. Click the "Start Analysis" button to start the analysis.

Ensure that the peak detection has worked as expected. The single electropherogram view is most suitable for checking peak detection.

If, in a region with many peaks close together, some peaks are not detected, decrease the minimum distance by clicking on the "Minimum Distance" parameter and setting the distance value from default 0.25 to 0.1 seconds, for example. Click "OK" to confirm this setting. If you do not need minimum distance between peaks, set the minimum distance value to 0 seconds.

Click the "Start Analysis" button again to start a new analysis according to this modified analysis profile.

In some cases, it may be necessary to repeat the adaptations to the analysis profile iteratively. If the peak detection worked as expected with the modified analysis profile, save this analysis profile and try to use this new profile instead of the "Default Fast Analysis" analysis profile for future "Fast Analysis" samples.

Note: Only users with user role "Advanced User" can modify and save parameters of an analysis profile. Users with user role "Basic User" can select another analysis profile, which is more suitable for the type of samples being analyzed.

After the analysis has been completed, the single electropherogram views of the analyzed samples will show the size of the detected DNA molecules in base pairs above the apex of the corresponding peaks.

The result table summarizes all properties QIAxcel ScreenGel software calculates for detected peaks. Right-click the header line of the table, select "Show column", and then select the property you are interested in. Alternatively, right-click the header line of the table and select "Show all columns". This option displays all the properties calculated by QIAxcel ScreenGel for each detected peak in the currently selected sample.

6.4.7 Analysis of RNA samples

This section describes how to analyze an RNA sample. It distinguishes between two different kinds of analyses: size and concentration determination and RNA quality control. For both analyses, perform steps 1–8. Then, switch to the subsection referring to the requested type of analysis.

1. Switch to RNA mode if this is not already selected. For details, refer to section Modes.
2. Load the samples you want to analyze using the "Experiment Explorer". For details, refer to the Loading sample data section.
3. If a size marker was run side by side with samples, create a new reference marker as described in Creating a reference marker.
4. Visualize the samples you want to analyze. See the Viewing sample data section for details on data inspection.
5. Select the samples to be analyzed.
6. Open the "Analysis" parameters panel to be able to specify the analysis properties.
7. Select the "Default RNA" analysis profile.

8. Analyze the RNA sample. Switch to one of the sections below according to your needs.

Continue with determination of size and concentration of RNA molecules, or quality control.

Determining the size and concentration of RNA molecules

1. In the reference marker section, check "Reference Marker Table" and select a previously saved reference marker.
2. Click the "Start Analysis" button to start the analysis.

   Ensure that the peak detection has worked as expected.

   If the first detected peak is not the alignment marker peak, as a first step, increase the alignment marker threshold. If this is not sufficient, add the parameter "Suspend Integration" and use the "Absolute" time unit to define the starting point as 0 minutes. Set the ending point of this parameter to shortly before the start of the alignment marker peak (e.g., set end to 2 minutes if the first alignment marker peak appears at 2.5 minutes).

   If the analysis profile is too sensitive and detects peaks where there is only noise, increase the threshold (e.g., from 2 S/N to 5 S/N).

   If the baseline follows the 28S peak, increase the baseline filter window size for roughly the last third of the migration time. This is done by clicking the "Add" button to add a second interval to the baseline filter parameter (e.g., set start to 6 minutes and the window size to 80 seconds).

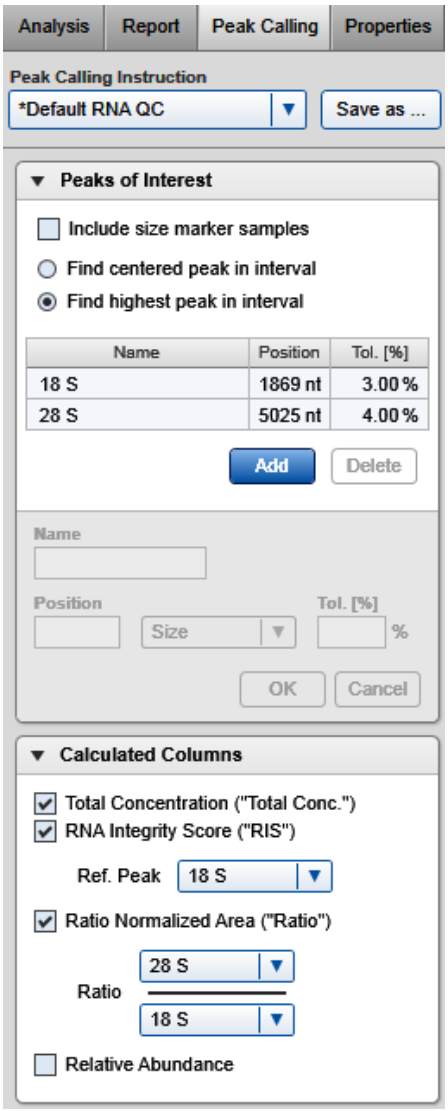
   Click the "Start Analysis" button again to start a new analysis according to this modified analysis profile.

   In some cases, it may be necessary to repeat the adaptations to the analysis profile iteratively. If the peak detection worked as expected with the modified analysis profile, save this analysis profile and try to use this new profile instead of the "Default RNA" analysis profile for future RNA analyses.
3. After the analysis has been completed, the single electropherogram views of the analyzed samples will show the size of the detected RNA molecules in nucleotides above the apex of the corresponding peaks.
   The correct concentrations can be examined in the peak result table. If the concentrations are not shown by default, right-click the header line of the table, choose "Show column" and then select the concentration column, which displays the concentrations in ng/µl. Alternatively, right-click the header line of the table and choose "Show all columns". This option displays all the properties calculated by QIAxcel ScreenGel for each detected peak in the currently selected sample.

Performing quality control of RNA, with a size marker

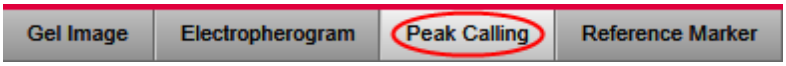
1. Perform steps 1 and 2 of the "Determine size and concentration of RNA molecules" section.
2. Switch to the "Peak Calling" tab of the parameters panel and select one of the provided peak calling instructions: "Default RNA QC", "Default RNA procaryote", or "Default RNA rat_mouse_human".

3. To determine the RNA integrity, select the "RNA Integrity Score" option and choose the 18S peak. To examine the 28S-to-18S-ratio in one sample, select the "Ratio Normalized Area" option and choose the 28S and the 18S peak. For prokaryotic RNA, choose the 23S and 16S peak, respectively. For detailed information on how to define peak calling instructions, refer to the section Modifying peak calling instructions.



Peak calling instruction for RNA QC.

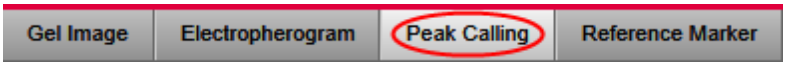
4. In the gel image overview, select all samples.
5. Click the "Start Peak Calling" button.
6. Inspect the peak calling result in the peak calling result overview.



Each row in this table represents the peak calling result for one sample. The RNA integrity score is given in the column "RIS". The 28S-to-18S-ratio, is given in the column "Ratio". In addition, the total concentration of RNAis given in the column "Total RNA concentration". Furthermore, for the 18S and 28S peak, it is listed whether or not this peak was found, based on the criterion given in the peak calling instruction. For detailed information on the peak calling result table, refer to the section Peak Calling.

Performing quality control of RNA, without the size marker

1. In the reference marker section, select "No Marker".
2. Click the "Start Analysis" button to start the analysis.
3. Ensure that the peak detection has worked as expected. For details on how to adjust the "Default RNA" analysis profile, see above.
4. Switch to the "Peak Calling" tab of the parameters panel and select one of the provided peak calling instructions: "Default RNA QC", "Default RNA prokaryote", or "Default RNA rat_mouse_human".
5. As the analysis was performed without the reference marker, adapt the peak calling instruction to search for peaks based on relative migration time instead of size. Click on the 18S peak and update the position criterion. Set the value to an average of the relative migration times that is shown in the result tables for the 18S peak of the selected RNA samples, change the unit to "Rel. Time", and save this setting by clicking the "OK" button. Adjust the tolerance parameter, if the relative migration times differ from sample to sample. Do the same for the 28S peak. For prokaryotic RNA, change the 23S and 16S peak, respectively. For detailed information on how to define peak calling instructions, refer to section Modifying peak calling instructions.
6. To determine the RNA integrity, select the "RNA Integrity Score" option and choose the 18S peak. To examine the 28S-to-18S-ratio in one sample, select the "Ratio Normalized Area" option and choose the 28S and the 18S peak.
7. In the gel image overview, select all samples.
7. Click the "Start Peak Calling" button.
8. Inspect the peak calling result in the peak calling result overview.



Each row in this table represents the peak calling result for one sample. The RNA integrity score is given in the column "RIS". The 28S-to-18S-ratio, is given in the column "Ratio". In addition, the total concentration of RNA is given in the column "Total RNA concentration". Furthermore, for the 18S and 28S peak, it is listed whether or not this peak was found, based on the criterion given in the peak calling instruction. For detailed information on the peak calling result table, refer to section Peak Calling.

6.4.8 Analysis of protein samples

This section describes how to analyze a protein sample. It distinguishes between two types of analysis: analysis of samples of low complexity (containing a single protein or few proteins); analysis of samples of high complexity, such as those containing multiple proteins from cell lysates. For both types of samples, perform steps 1–6. Then switch to the subsection referring to the requested type of analysis.

1. Switch to Protein mode if this is not already selected. For details, refer to section Modes.
2. Load the samples you want to analyze using the "Experiment Explorer". For details, refer to the Loading sample data section.
3. If a size marker was run side by side with samples, create a new reference marker as described in Creating a reference marker.
4. Visualize the samples you want to analyze. See the Viewing sample data section for details on data inspection.
5. Select the samples to be analyzed. See Selecting samples for analysis or report section for details.
6. Open the "Analysis" parameters panel to specify the analysis properties. These depend on the content of the sample being analyzed. Therefore, switch to one of the following subsections according to your needs.

Continue with the analysis of samples of low or high complexity (see below).

Analyzing samples of low complexity

1. Select the "Default Protein" analysis profile.
2. In the reference marker section, check "Reference Marker Table" and select a previously saved reference marker.
3. Click the "Start Analysis" button to start the analysis.

   Ensure that the peak detection has worked as expected. The single electropherogram view is most suitable for checking peak detection.

   If there are system peaks that do not belong to the sample, use the suspend integration parameter to avoid peak detection in a region where no peaks are expected. To apply this parameter, click the "Add" button in the analysis properties section to add a new parameter to the selected analysis profile. Select "Suspend Integration" and set the start and end values for defining the region where to avoid peak detection. In case only one sample is analyzed, select "Absolute" time as the unit because it may be easier to define the correct region in minutes. If system peaks reproducibly occur at the same migration times and multiple samples are analyzed at once, try to define a "Suspend Integration" parameter with the start and end given in relative time units, because relative time is more comparable across samples.

   Note: If it is not possible or quite difficult to define a "Suspend Integration" parameter, use the "Delete Peak" feature after analysis of the sample in the single electropherogram view.

   Click the "Start Analysis" button again to start a new analysis according to this modified analysis profile, but note that manually deleted peaks will be detected again.

   In some cases, it may be necessary to repeat the adaptations to the analysis profile iteratively. If the peak detection worked as expected with the modified analysis profile, save this analysis profile and try to use this new profile instead of the "Default Protein" analysis profile for future protein analyses.
4. After the analysis has been completed, the single electropherogram views of the analyzed samples will show the size of the detected proteins in kilodalton (kD) above the apex of the corresponding peaks.
   In protein mode, the column "Rel. Conc. [ng/µl]" displays the relative concentration for each detected peak. As for all peaks, the same reference is used to calculate the relative concentration. Since the binding of the dye differs from one protein species to another, the concentration can only be given as a relative concentration. This value can be used to compare relative concentrations of corresponding proteins (same migration time) across different samples.

If this column is not shown, right-click the header line of the table, select "Show column", and then select the "Rel. Conc. [ng/µl]" column. Alternatively, right-click the header line of the table and select "Show all columns". This option displays all the properties calculated by QIAxcel ScreenGel software for each detected peak in the currently selected sample.

Analyzing samples of high complexity, such as cell lysates

1. Select the "Protein Lysate" analysis profile.
2. In the reference marker section, check "Reference Marker Table" and select a previously saved reference marker.
3. Click the "Start Analysis" button to start the analysis.

   Ensure that the peak detection has worked as expected. The single electropherogram view is most suitable for checking peak detection.

   As the analyzed sample is of high complexity, usually a lot of peaks are detected. Nevertheless, if there are system peaks in the sample, remove them using "Suspend Integration" as described in the section above.

   If the baseline follows the signal, increase the baseline filter window. This is done by clicking on the parameter value and changing the window size (e.g., to 180 seconds). Then click the "OK" button.
   If the baseline starts following the signal at a later migration time, click on the "Add" button in the analysis properties section to add a new parameter to the selected analysis profile. Select "Baseline Filter", set the start value to a later migration time, and set an increased window value. Then click the "OK" button.

   Click the "Start Analysis" button again to start a new analysis according to this modified analysis profile.

   In some cases, it may be necessary to repeat the adaptations to the analysis profile iteratively. If the peak detection worked as expected with the modified analysis profile, save this analysis profile and try to use this new profile instead of the "Protein Lysate" analysis profile for future protein analyses.
4. Examine the results as described in point 4 in the section above.

Examining samples derived from cell lysates or samples containing multiple proteins

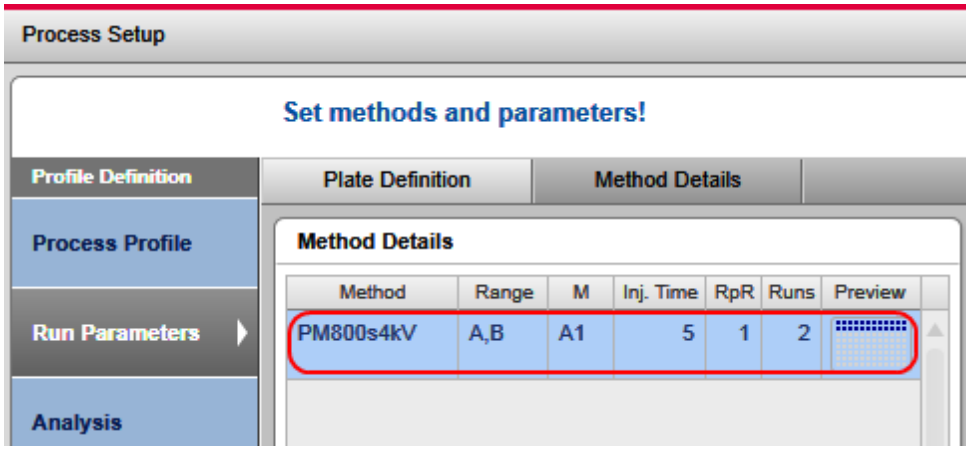
1. Select all samples of interest and analyze these samples with the same analysis profile, as described above.
2. Switch to the peak calling tab and create a new peak calling instruction by selecting "NewPeakCallingInstruction" in the peak calling instruction drop-down list.
   Click the "Add" button to define search criteria for your peak of interest. Define the name of your protein of interest in the "Name" field and its size (e.g., 26 if the protein is 26 kD) in the "Position" field and select "Molec. Mass" as unit. Select a tolerance value to allow a flexible search. Enable "Relative Abundance" in the "Calculated Columns" section. Click "OK".
3. Click the "Start Peak Calling" button to start the peak calling.
4. Examine the results in the peak calling result table.

   This table lists the results for each sample in a separate row. The columns refer to whether the peak of interest was found in the respective sample and display the calculated properties in case the peak of interest was found.
5. The column "Relative Abundance" shows how much of the protein corresponding to the sought peak is contained in each sample relative to the other samples. The relative abundance value is given in percentage. For the sample containing the largest concentration of this protein, the relative abundance is 100%. If, for another sample, a relative abundance of 50% is given, the second sample contains half the amount of the protein of interest of the first sample (e.g., first sample contains 2 ng/µl and second sample contains 1 ng/µl).

   Note: Because in complex samples, many proteins are detected at the same time, peaks may overlap. Consequently, the relative quantification of proteins in complex samples is less accurate compared to the relative quantification of proteins in samples of low complexity.

Determining the absolute quantification of proteins

1. The absolute concentration of a protein can be calculated if the same protein species of known concentration (reference protein) has been analyzed side by side with samples under the same conditions, and using the same sample buffer.

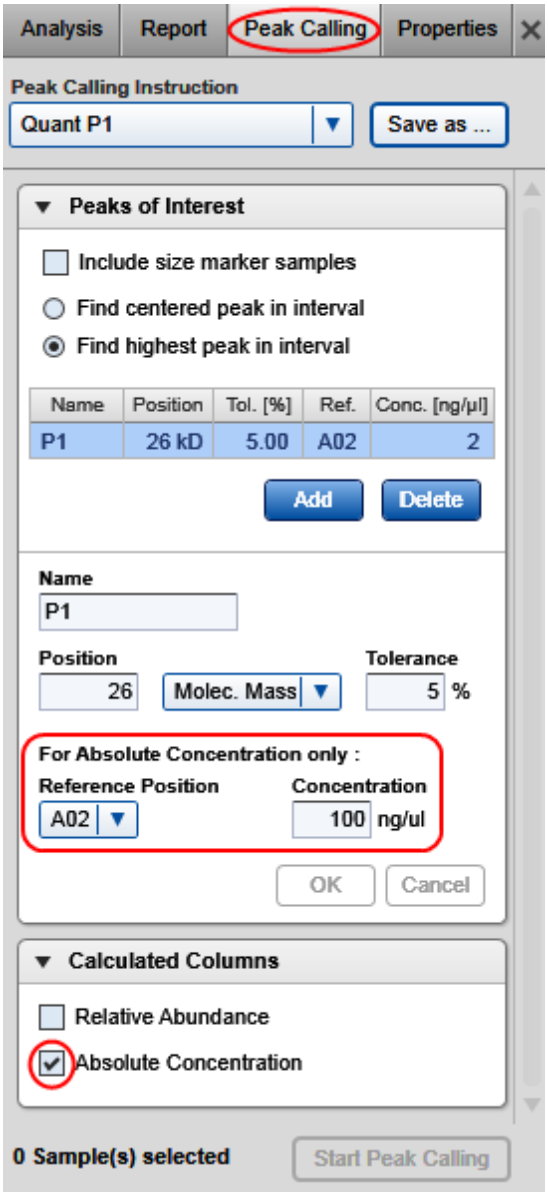


Run definition for rows A and B.

This means that the reference protein and the samples must be separated using the same method. In the image above, the reference protein must be provided in one of the positions in row A or row B, excluding position A1, which contains the size marker.

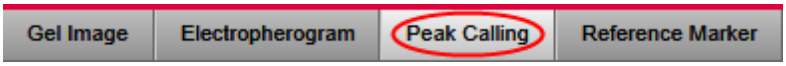
2. Select all samples of interest, including the reference protein, and analyze these samples with the same analysis profile as described above.
3. Switch to the peak calling tab and create a new peak calling instruction by selecting "NewPeakCallingInstruction" in the peak calling instruction drop-down list.

   Click "Add" to define search criteria for your peak of interest. Define the name of your protein of interest in the "Name" field and its size (e.g., 26 if the protein is 26 kD) in the "Position" field and select "Molec. Mass" as unit. Select a tolerance value to allow a flexible search. Define the plate position (e.g., A2) and the concentration of the reference protein.



Peak calling instruction for absolute quantification.

   Enable "Absolute Concentration" in the "Calculated Columns" section. Click "OK".
4. Click the "Start Peak Calling" button to start the peak calling.
5. Examine the results in the peak calling result table.



This table lists the results for each sample in a separate row. The columns refer to whether or not the peak of interest was found in the respective sample and display the calculated properties in case the peak of interest was found.

The column "Abs. Conc. [ng/µl]" shows the absolute concentration value. The sample representing the reference protein displays the reference concentration in a bold font.

Note: The absolute concentration will be calculated only if the the sample representing the reference protein is part of the selection for peak calling, and the peak of interest is found in the sample and in the reference as well. If the absolute concentration could not be calculated, "n/a" is displayed.

Note: As QIAxcel ScreenGel software is able to determine protein sizes in the range from 10 to 100 kD, smaller or larger proteins are not annotated with a size value. Instead "n/a" is displayed above the corresponding peaks.

6.4.9 Manually modifying analysis results

The QIAxcel ScreenGel software algorithms analyze the data fully automatically. The user can only influence the automated analysis through the analysis parameters.

After the analysis, the results can be modified manually by the user.

6.4.9.1 Modifying the threshold

In the single electropherogram view, the threshold parameter can be interactively changed by moving the threshold with the mouse. When doing so, the sample is reanalyzed using the analysis parameters of the sample properties and the new threshold value.

6.4.9.2 Deleting a peak

Deleting a peak is possible in the "Single Electropherogram View" only.

To delete a peak, proceed as follows:

1. Switch to the "Single Electropherogram View".
2. Right-click the top of the peak in the electropherogram and select "Delete Peak" from the context menu that appears. The peak will be deleted.

Note: After new analysis, the peak can be detected again depending on the analysis parameters. Repeat the steps above to delete it again.

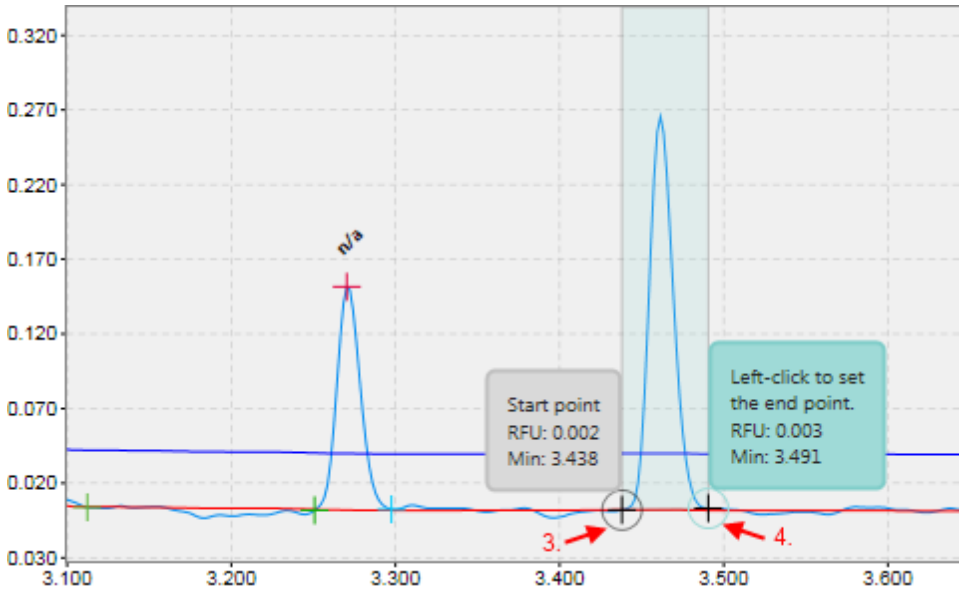
Note: A peak can be deleted by users with the assigned user roles "Basic User" and "Advanced User" only.

6.4.9.3 Adding a peak

Adding a peak is possible in the "Single Electropherogram View" only.

To add a peak, proceed as follows:

1. Switch to the "Single Electropherogram View".
2. Right-click the electropherogram and select "Insert Peak" from the context menu that appears.
3. A marker is displayed that moves along the signal while the mouse is being moved. Move the marker to the left border of the peak that is to be added. Left-click to set the left border.
4. Accordingly, left-click to set the right border of the peak to be added. If a peak can be found in the marked area, the peak is added to the result table and the visualization is updated.



Specifying the peak area.

Note: Adding a peak before the first alignment marker peak or after the second alignment marker peak is only possible if the signal rises above the alignment marker threshold in the corresponding region.

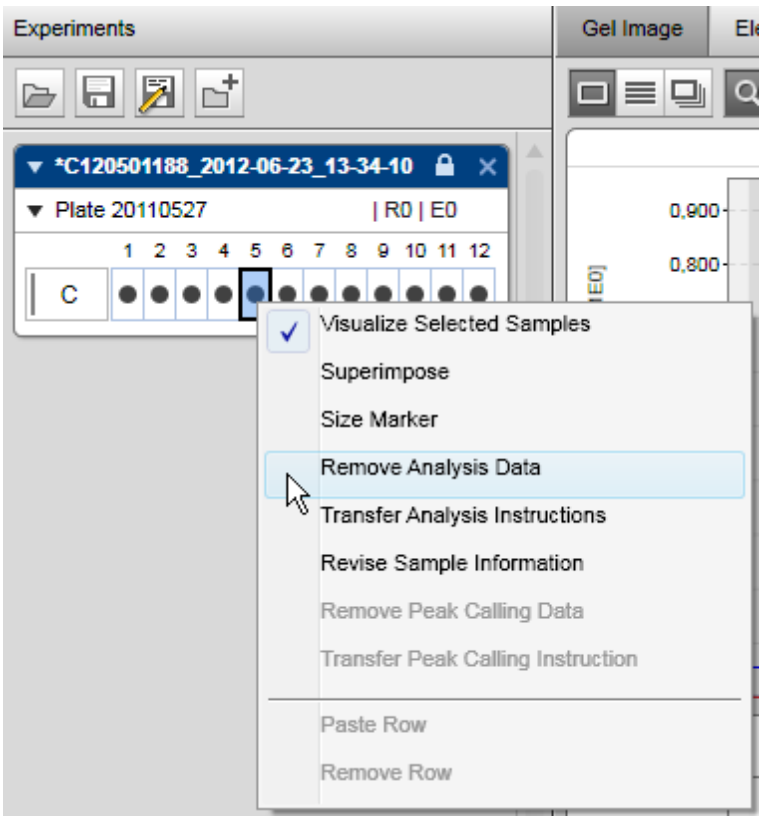
Note: A peak can be added by users with the assigned user roles "Basic User" and "Advanced User" only.

6.4.9.4 Removing analysis results

Removing the analysis result from samples is only possible using the "Experiment Explorer".

To remove the analysis result from samples:

1. Select the samples in the "Experiment Explorer". Refer to the Selecting samples section for information about how to select multiple samples.
2. Right-click the selection and select "Remove Analysis Data" from the context menu that appears.



Removing the analysis result of C5.

The result tables for these samples become empty. The representation of the sample in gel image and electropherogram view is updated: all peak annotations as well as baseline and threshold lines disappear.

Note: Only users with the assigned user roles "Basic User" and "Advanced User" can remove analysis results.

6.4.9.5 Checking alignment marker

To check the alignment marker of a sample:

1. Select the sample in the "Experiment Explorer".
2. View the sample properties at the right side of the "Analysis" environment, in the "Analysis Instructions" panel. Refer to Inspecting sample properties for detailed information about how to view the properties.
3. Check if the alignment marker of the sample is correct.
   If not, the alignment marker of a plate can be changed. In the "Experiment Explorer", right click the plate name. Select the context menu option "Overwrite alignment marker". Select the correct alignment marker in the "Overwrite Marker" dialog box that appears and confirm by clicking "OK".

Note: To ensure analysis compatibility, the reference marker drop-down list contains only reference marker tables that match the alignment marker of the samples.

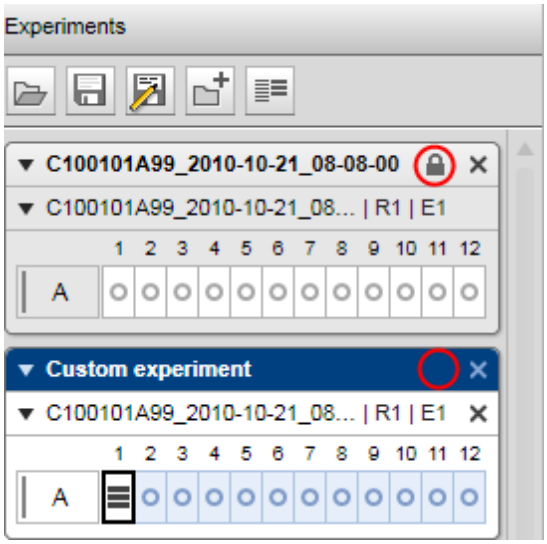
6.4.10 Customizing experiments

Experiments are created automatically from every process. Additionally, the user can create and modify experiments. This allows the user to compare samples from different experiments, and even different processes.

Note: Creating and modifying customized experiments requires the user role "Advanced User".

A customized experiment may contain single rows or groups of rows as well as plates. However, within the experiment all rows will be still grouped in plate(s). Every time a row or plate is added to an experiment you get a copy of it. This means that the source experiment, from which the row/plate originates, will remain unaffected by all changes within the target experiment.

Note: You can modify the composition of customized experiments only. The composition of an experiment, which is the automatic result of a process cannot be modified (see the image below.)



Run results are marked with a padlock symbol. Custom experiments are not marked.

For general information about handling experiments and the "Experiment Explorer", see the Handling samples and experiments section.

6.4.10.1 Creating a new experiment

To create a new customized experiment:

1. Click at the top of the "Experiment Explorer".
2. Enter a unique name for the new experiment into the edit field of the dialog box that appears and click "OK".

   Important: The experiment name cannot be changed later.
3. A new empty experiment will be created and displayed in the "Experiment Explorer" as the last experiment, at the bottom.

   Use the scrollbar of the "Experiment Explorer" if the new experiment is outside the view. The new experiment will be activated automatically. If the previously active experiment was modified, the system asks you whether to save the changes or not. For more details about activating and deactivating see the Activating an experiment section.

Refer to the Modifying an experiment section for information about how to collect samples for the new experiment.

Note: The composition of this experiment can be modified at any time, in comparison to experiments automatically generated by a process.

Note: New experiments can be created by users with the assigned user role "Advanced User" only.

6.4.10.2 Modifying an experiment

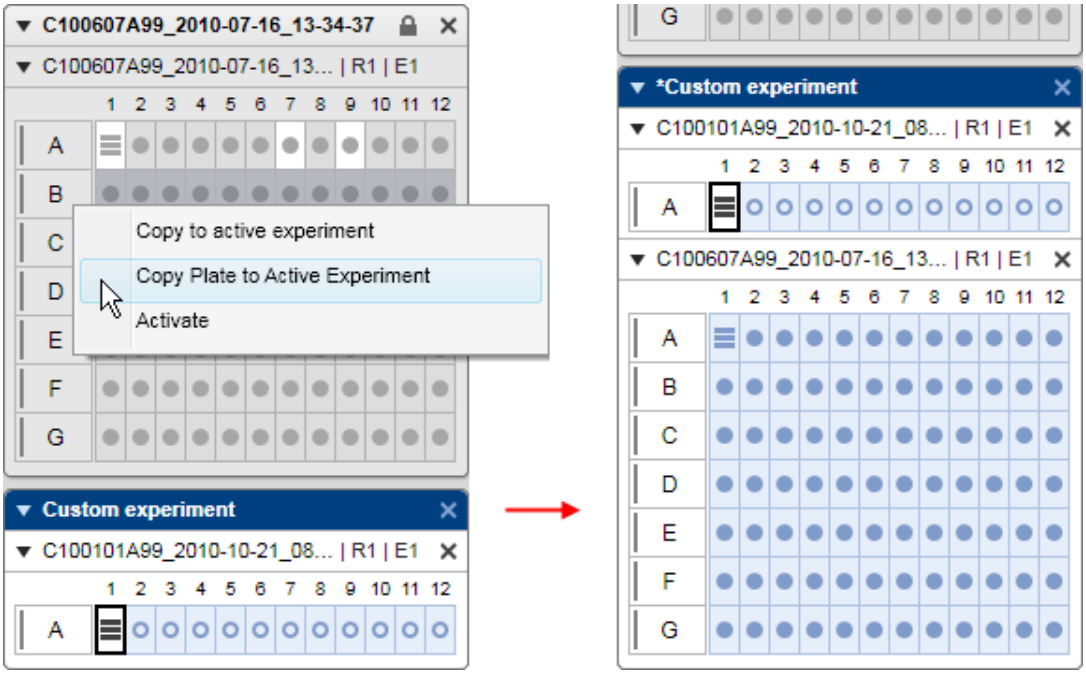
If a customized experiment should be modified, make sure that it is activated. For more details about activating an experiment see the Activating an experiment section.

Note: Only the composition of customized experiments can be modified. The composition of an experiment that is the automatic result of a process cannot be modified, and therefore the context menu options described below are disabled.

To modify an experiment:

1. Load the source experiment that contains the samples. For further details on loading, see the Loading samples section.
2. Create or activate the experiment that is to be customized in the "Experiment Explorer".
3. Expand the source experiment so that the required plates and rows are visible. The experiment can be expanded without activating. For more details about expanding see the Expanding and collapsing section.
4. Modify the experiment as required:

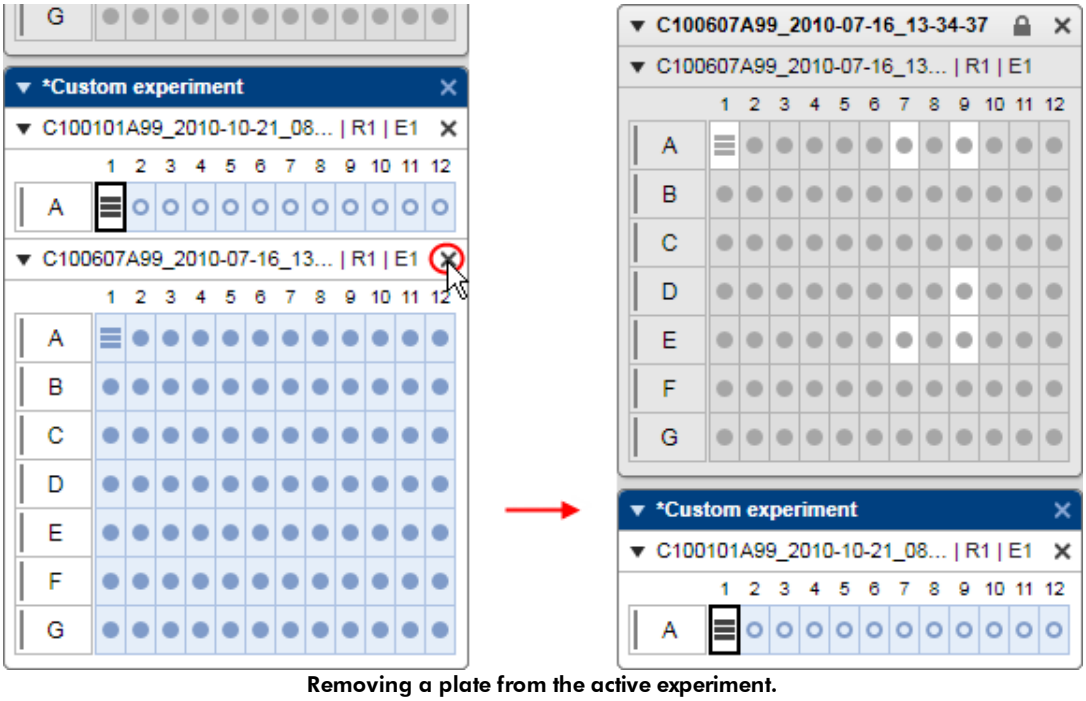
- To add a plate to the active experiment, right-click the plate to add and select the context menu option "Copy Plate to Active Experiment". A copy of the plate will be created and added to the active experiment at the bottom.



Adding a plate to the active experiment.

Note: The complete plate will be copied to the experiment, the original plate stays unchanged. So any further modification of this plate in the active experiment does not affect the original plate.

- To remove a plate from the active experiment, click the "Close" button of the plate. The plate will disappear from the experiment.



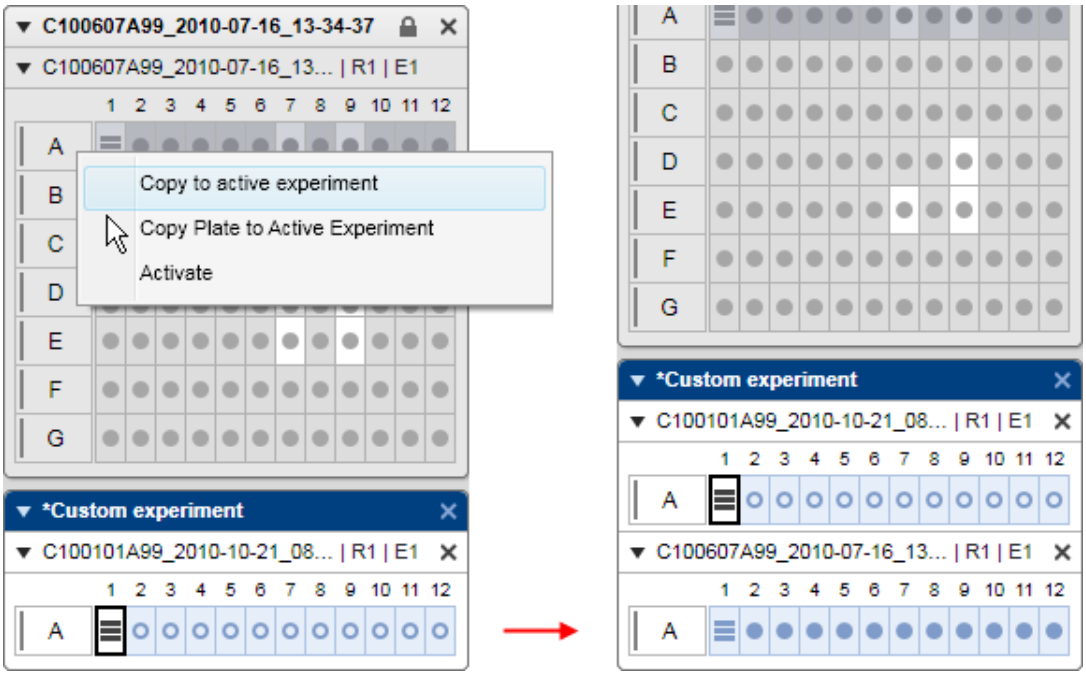
Removing a plate from the active experiment.

Note: This plate will be removed only from the active experiment, the original plate remains unchanged.

- Adding a row is similar to adding a plate. Place the mouse cursor over the row to add to the active experiment and select the menu item "Copy to Active Experiment".

  To preserve the context of the row, a copy of its plate will be created and added to the active experiment containing a copy of the selected row. If you add another row from the same plate to the active experiment, a copy of the row will be created and added to the copy of the plate inside the active experiment.

  Multiple rows of the same plate can be added in a similar way, but by simultaneously holding the "Shift" or "Ctrl" key during selection.



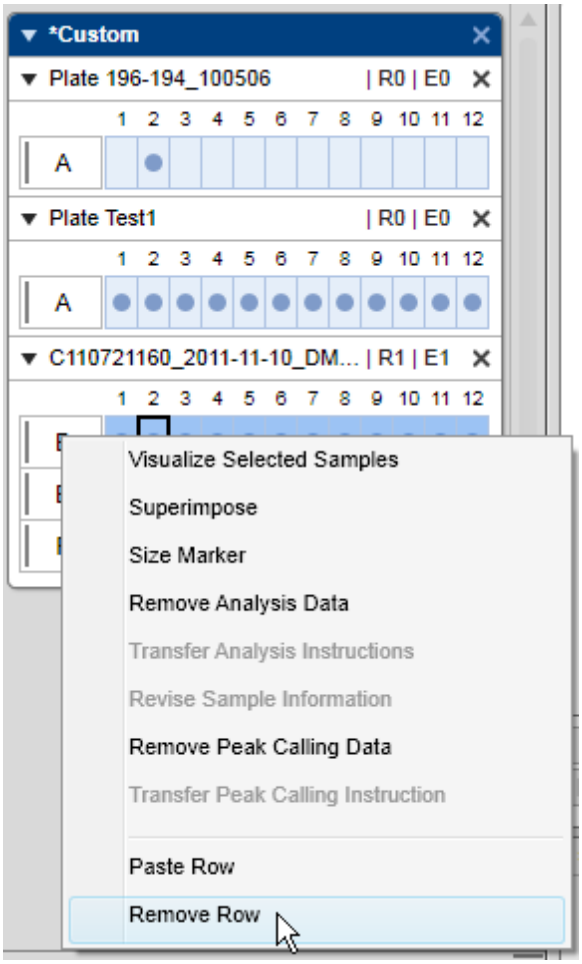
Adding a row to the active experiment.

Note: A row can be located in the experiment only once.

Note: Individual samples cannot be added to the active experiment. Add the complete row instead, but visualize the required samples only.

An alternative way to add a row is to copy and then paste the row into the active experiment. To do this, right-click the row you want to add and select the context menu option "Copy Row". Then, right-click the active experiment and select the option "Paste Row" from the context menu. The row will be copied to the active experiment as described above.

- To remove a row from the active experiment right-click the row letter and select the option "Remove Row" from the context menu. The row will be removed from the active experiment. If the plate contains only one row, you cannot remove it; instead, please remove the plate.


*Custom
Plate 196-194_100506 | R0 | E0
1 2 3 4 5 6 7 8 9 10 11 12
A
Plate Test1 | R0 | E0
1 2 3 4 5 6 7 8 9 10 11 12
A
C110721160_2011-11-10_DM... | R1 | E1
1 2 3 4 5 6 7 8 9 10 11 12
Visualize Selected Samples
Superimpose
Size Marker
Remove Analysis Data
Transfer Analysis Instructions
Revise Sample Information
Remove Peak Calling Data
Transfer Peak Calling Instruction
Paste Row
Remove Row

Removing a row from the custom experiment.

6.4.11 Report/Export

The analysis environment provides a flexible and powerful tool for reporting (RTF or PDF format) and data export (XML format).

For convenient reuse, corresponding report and export configurations can be stored together in report/export profiles. Thus, both reporting and data export may be integrated to form a fully automated process by including a report/export profile into a process profile.

You can specify which information is to be included in the report and export, individually. The report and export files can be customized to suit your needs.

Each report contains of two main sections:

- The "overview section" for information about all samples, such as a gel overview
- The "sample details" section for detailed information about each sample

In the "sample details" section, the information related to each sample is reported for each sample grouped in the following subsections:

- Sample Header
- Sample Graphics
- Result Table
- Run Parameter

- Analysis
- Reference Marker

The order of the samples is the same as in the view.

For further details on customizing reports and export, see the Modifying a report/export profile section.

6.4.11.1 Generating a report

The basic procedure of manually generating a report in the "Analysis" environment is as follows:

1. Load the samples using the "Experiment Explorer".
   For further details on loading sample data, see section Loading sample data.
2. Inspect the samples before reporting.
   See the Viewing sample data section for more details on data inspection.
   For this step, the "Gel view" or the "Electropherogram overview" are especially useful.
3. Select the samples you want to report.
   For further details on selecting samples, see section Selecting samples for analysis or report
4. Select report settings and start reporting.

   On the right-hand side of the analysis environment, the report toolbar can be found.

   If it is not visible, you can display it using the "View" menu (selecting the menu item "View"/"Show Analysis Parameters") or by clicking the icon at the extreme right of the view selection bar:

   Select the "Report" tab of the toolbar.

   Select a predefined report/export profile. The report settings of the selected profile are shown below the drop-down list. For details refer to the Report options section.

   Make sure that at least one of the report formats "PDF" or "RTF" is selected. Additionally, ensure that at least one of the options ("Overview" or "Sample Details") is selected. If not, select another predefined report/export profile. (Users assigned the user roles "Advanced User" or "Basic User" may modify the settings as they wish.)

   Specify the directory where the report files will be saved (refer to section Modifying a report/export profile for information on how to specify the report directory).

   Click the "Start Report/Export" at the bottom of the "Report" tab to start reporting.

   Note: The button "Start Report/Export" is disabled if no samples are selected in the view (see Step 3).

   The report files will be generated automatically and stored in the specified directory.

   If you have selected the "Print report" option the report will be printed on the default printer.

   Note: Ensure that you have defined a default printer on your system.
5. Inspect the report files.

   If the options "Display Report" and "PDF" were selected, the generated report will be opened automatically in the default PDF reader.

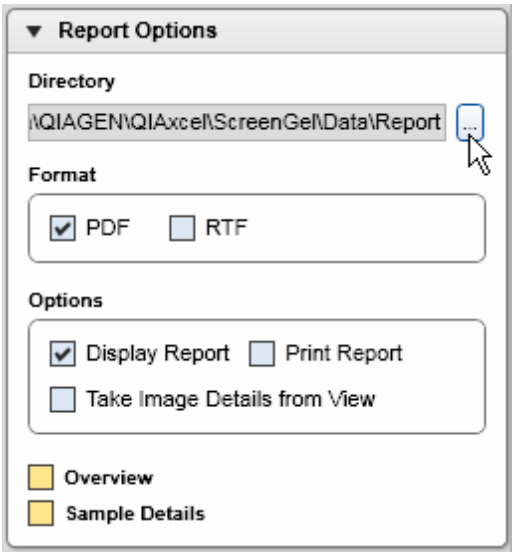
6.4.11.2 Report options

The report/export settings are divided into two groups:

- "Report Options"; contains the report settings
- "Export Options"; contains the export settings

Note: You can collapse and expand each group by clicking ▼ and ▶ to the left of the group name.

"Report Options"



"Report options".

The options are described below.

Directory	Select the directory in which the generated report file should be stored by clicking . In the dialog that appears, navigate to the correct directory and click "OK".
PDF	A file in PDF format will be generated.
RTF	A file in RTF format will be generated. You can select both formats.
Display Report	If you select this option and the format option "PDF" is selected, the generated report will be displayed automatically using the default PDF reader.
Print Report	If you select this option the generated report file(s) will automatically be sent to the default printer. **Note:** Ensure that you have a default printer on your system.
Use Images as Displayed	Use this option to obtain images that look similar to the presentation in the QIAxcel ScreenGel software regarding alignment, scales, labels, zoom, etc. **Note:** This option is available in the analysis environment only, it may not be used in a process profile.
Overview	The report contains of an overview section.
Sample Details	The report contains of a sample section.

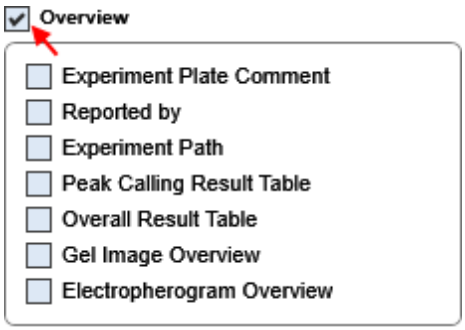
Note: If one of the check boxes "PDF or "RTF" is checked, the report/export profile is valid only if either the "Overview" or "Sample Details" check box is selected additionally.

Overview section

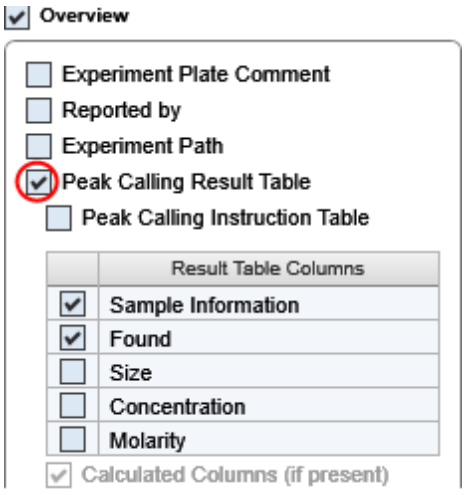
If the "Overview" option is selected, the following information is included automatically to the overview section of the report:

Report Date	Date and time of report generation.
Experiment Name	Name of the experiment the sample data belong to.
Cartridge ID	ID(s) of the cartridge(s) that the samples were processed with.
Cartridge Expiration Status	This information is automatically included if the cartridge has exceeded its expiration date.
Calibration Status	Calibration status of the cartridge(s) at process time.
Instrument ID	Serial number of the instrument(s) used to process the samples.
Data Acquisition Status	Only in case of an incomplete experiment. Gives information about planned and performed runs (e.g., 2 out of 8 runs performed successfully).
Corrupt Experiment Accepted by	Only in case of an incomplete experiment, which was accepted by a user. Name of the user who has accepted the experiment.
Corrupt Experiment Accepted on:	Only in case of an incomplete experiment, which was accepted by a user. Date and time when the experiment was accepted.

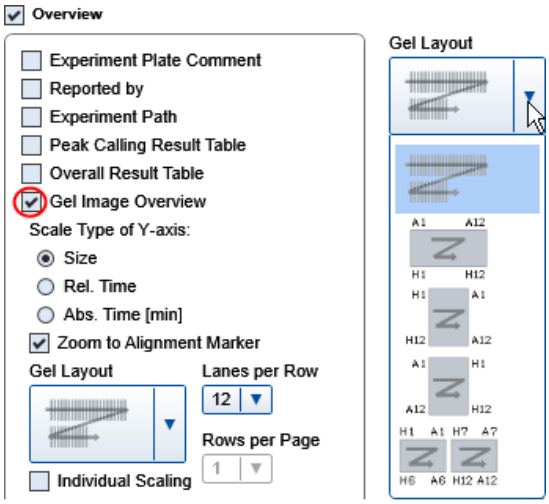
Select the following optional information that you want to include into the overview section:



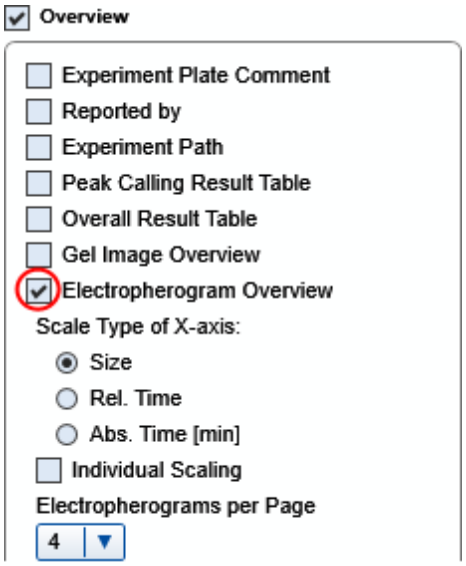
Optional overview information.



Special options for "Peak Calling Result Table"



Special options for "Gel Overview".



Special options for "Electropherogram Overview".

The optional fields are described on the next page.

Experiment Plate Comment	Experiment plate comment.
Reported by	The ID of the user who generated the report/export.
Experiment Path	The path where the experiment is stored.
Peak Calling Result Table	The peak calling result overview table will be included. Additional options are selectable (see picture above).

Peak Calling Instruction Table	Select this option to include the peak calling instruction table to the peak calling result overview table.
Sample Information	Select this option to include the "Sample Information" column in the peak calling result overview table.
Found	Select this option to include the "Found" column for each peak of interest to the peak calling result overview table.
Size	For DNA and RNA mode only. Select this option to include the "Size" column for each peak of interest in the peak calling result overview table.
Molecular Mass	For protein mode only. Select this option to include the "Molecular Mass" column for each peak of interest in the peak calling result overview table.
Concentration	For DNA and RNA mode only. Select this option to include the "Concentration" column for each peak of interest in the peak calling result overview table.
Relative Concentration	'For protein mode only. Select this option to include the "Relative Concentration" column for each peak of interest in the peak calling result overview table.
Molarity	For DNA and RNA mode only. Select this option to include the "Molarity" column for each peak of interest in the peak calling result overview table.

Note: Calculated columns (such as "Ratio", "RIS", "Absolute Concentration") are automatically included, if they are part of the applied peak calling instruction.

Note: If there are too many peaks of interest, the table is split between two peaks of interest, The sample info and the calculated columns appear only in the first table, the following tables are marked with "(continued)" in the header.

Note: If samples to which different peak calling instructions were applied are selected, a new table starts for each peak calling instruction. Additionally, if samples from different plates are selected, a new table starts for each plate.

Overall Result Table

Use this option to include a result table for size and concentration results of all samples of a plate. If there are samples from different plates selected, one result table for each plate will be created. Each sample represents a row. The table columns are: sample information, size, and concentration repeated for each peak of the sample.

Note: If the samples have no sample information, the position is printed instead. If the sample has too many peaks, the remaining peaks are printed in a further row, with an empty sample information/position column.

Note: If samples from different plates are selected, a new table starts for each plate.

Gel Image Overview

If you select this option, the gel image of all selected samples will be included.

Note: The gel image in the report will have the left-hand y-axis on both sides, also if the "Use Images as Displayed" option is selected.

Additional options appear to specify the gel layout (see picture above):

Scale type of the Y-axis

If you select "Size" (in DNA and RNA mode) or "Molecular Mass" (in protein mode), respectively, the y-axis will show a size scale based on the reference marker on both sides of the gel image, also if the "Use Images as Displayed" option is selected. The lanes in the gel image will be aligned according to the alignment markers.

Note: The size scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed with the same reference marker table, and the alignment markers have been correctly identified. Otherwise, the y-axis will show relative migration time, if possible.

If you select "Rel. Time", the y-axis will show relative migration time. The lanes in the gel image will be aligned according to the alignment markers.

Note: The relative time scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the lanes cannot not be aligned and the y-axis will show an absolute time scale.

If you select "Abs. Time [min]", the lanes will not be aligned and the y-axis will show an absolute time scale.

Note: This option is not available if the "Use Images as Displayed" option is selected.

Zoom to Alignment Marker

Select this option, if available, to scale the lanes so that the lanes start with the lower alignment maker band and end with the upper alignment marker band (crop data outside of the alignment markers).

Note: This is possible only if all samples are analyzed.

		Note: This option is not available if the "Use Images as Displayed" option is selected.
	Standard layout	Specify the number of lanes per row: 4, 6, 8, 12, 16, 24, 32, 36, or 48. The lanes are printed from left to right as shown by the first layout pictogram. The lane order is the same as in the view. The lanes are labeled with sample position, sample information, plate ID, run number, and entry number. Use this option if you intentionally changed the lane order.
	Horizontal plate layout	The lane order is fixed according to the positions of a plate, starting with A1 at the upper left and ending with H12 at the lower right. Positions for samples not selected remain empty. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
	Vertical plate layout	The lane order is fixed, starting with H1 at the upper left and ending with A12 at the lower right. Positions for samples not selected remain empty. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
	Reverse vertical plate layout	The lane order is fixed, starting with A1 at the upper left and ending with H12 at the lower right. Positions for samples not selected remain empty **Note:** This option is not available if the "Use Images as Displayed" option is selected.
	Split plate layout	The lane order is fixed. The vertical plate layout is split as shown in the last pictogram. Positions for samples not selected remain empty. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
	Rows per Page	Use this option to specify the number of rows to be printed on one page. **Note:** This option is not available if the "Standard layout" option is selected. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
	Individual Scaling	For all gel overview layouts. Select this option to auto-scale the contrast for each gel lane individually. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
Electropherogram Overview		If you select this option the electropherogram overview for all selected samples will be included. The order is the same as in the view. If a sample is analyzed, all detected peaks are marked (red apex, green apex for alignment markers).

Scale Type of the X-axis	If you select "Size" (in DNA and RNA mode) or "Molecular Mass" (in protein mode), respectively, the x-axis will show a size scale based on the reference marker. The electropherograms will be aligned according to the alignment markers. **Note**: The size scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed with the same reference marker table, and the alignment markers have been correctly identified. Otherwise, the x-axis will show relative migration time, if possible. If you select "Rel. Time", the x-axis will show relative migration time. The electropherograms will be aligned according to the alignment markers. **Note**: The relative time scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the electropherograms will not be aligned and the x-axis will show an absolute time scale. If you select "Abs. Time [min]", the electropherograms will not be aligned and the x-axis will show an absolute time scale. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
Zoom to Alignment Marker	Select this option, if available, to scale the electropherograms so that the electropherograms start with the lower alignment maker peak and end with the upper alignment marker peak (crop data outside of the alignment markers). **Note:** This is possible only if all samples are analyzed. **Note:** This option is not available if the "Use Images as Displayed" option is selected.

Individual Scaling	Select this option to auto-scale the y-axis for each electropherogram individually. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
Electropherograms per page	For the "Electropherogram Overview" specify the number of electropherograms per page. This option affects only the height of the electroperogram image. The width is not changed.

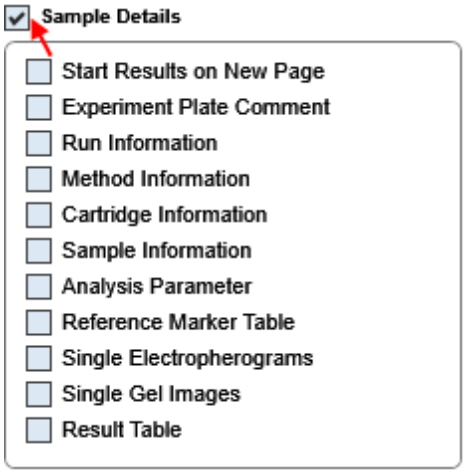
Note: In RNA mode, if you want the 28 S/18 S ratio to be included in the report, select the the overview option "Peak Calling Result Table" (refer to Analyze RNA samples for information how to analyze RNA samples).

Sample details section

The following information is included automatically for each sample:

Information	Description	Report section
Experiment Name	Name of the experiment the sample data belong to.	Sample header
Plate ID	ID of the plate the sample belongs to.	Sample header
Position	Sample position on the plate.	Sample header
Run Number	If the same sample was processed multiple times, this number identifies the run that produced the sample data (for detailed information, refer to Run parameters and result structure).	Sample header
Run Entry Number	The run entry number of the plate (for detailed information, refer to Run parameters and result structure) .	Sample header
Run Date	Date and time the process was started.	Run
Instrument ID	Serial number of the instrument the sample was processed with.	Run

Select the following optional information that you want to include in the sample section:



Optional sample details.

The optional fields are described below.

Start Results on New Page	If you select this option, the results for each sample will start on a new page.	
Experiment Plate Comment	If you select this option, the experiment plate comment is included in the "Sample Header" section.	
Run Information	If you select this option, the following information is included in the "Run" section of the sample:	
	Rise time	The parameter for the applied Bessel filter (see also Settings).
	Applied injection time	The applied sample injection time. **Note:** This time can differ from the methods sample injection time if there was another sample injection time specified in the process profiles run parameters. (see Selecting run parameters).
	Applied separation time	The applied separation time during method run. **Note:** This time can differ from the methods separation time if the user adjusted the separation time during run.
	Processed by	The ID of the user who processed the sample.
Method Information	If you select this option, the following information is included in the "Run" section:	
	Applied method	Name of the method the sample was processed with.
	Method injection time	Sample injection time as it was defined in the method.
	Method injection voltage	Sample injection voltage as it was defined in the method.
	Method separation time	Separation time as it was defined in the method.
	Method separation voltage	Separation voltage as it was defined in the method.
Cartridge Information	If you select this option, the following information will be included in the "Run" section:	
	Cartridge ID	ID of the cartridge the sample was processed with.
	Cartridge Calibration Status	Calibration status of the cartridge at process time: "OK", "Not calibrated", or "Conditional OK". For information on calibration status, refer to section Running the calibration wizard.

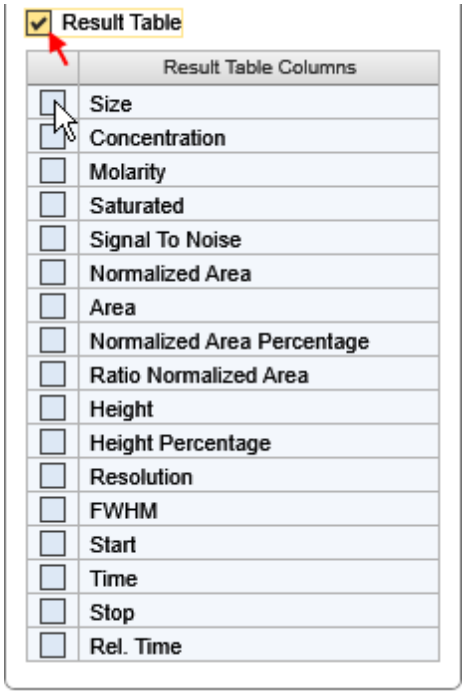
	Cartridge Expiry Date	The expiration date of the cartridge that was used for sample processing.
Sample Information	The sample information is included to the "Sample Header" section.	
Analysis Parameter	The analysis parameters applied to the sample will be included in the report section "Analysis".	
Reference Marker Table	The reference marker table used during analysis will be included.	
Electropherogram Single View	The electropherogram will be included. If the sample has been analyzed, baseline, threshold line, and peak markers (start, stop, red apex, green apex for alignment markers) are included. Additionally, peak labels are included showing the peak size, if determined, otherwise the relative migration time. Use the "Use Images as Displayed" option to print the electropherogram as displayed. Additional options appear to specify the single electropherograms. **Note:** If the "Use Images as Displayed" option is selected, the gel lane is combined with the electropherogram if it is visible in the QIAxcel ScreenGel software.	
	Scale Type of X-axis	If you select "Size" (in DNA and RNA mode), or "Molecular Mass" (in protein mode), respectively, the x-axis will show a size scale based on the reference marker, if the sample has been analyzed with a reference marker table and the alignment markers have been correctly identified. Otherwise, the x-axis will show relative migration time, if possible. If you select "Rel. Time", the x-axis will show relative migration time, if the sample has been analyzed and the alignment markers have been correctly identified. Otherwise, the x-axis will show an absolute time scale. If you select "Abs. Time [min]", the x-axis will show an absolute time scale. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
	Zoom to Alignment Marker	Select this option, if available, to scale the electropherograms so that the electropherograms start with the lower alignment maker peak and end with the upper alignment marker peak (crop data outside of the alignment markers). **Note:** This is possible only if all samples are analyzed. **Note:** This option is not available if the "Use Images as Displayed "option is selected.
	Individual Scaling	Select this option to auto-scale the y-axis for each electropherogram individually. **Note:** This option is not available if the "Use Images as Displayed" option is selected.

Gel Single View	The gel lane will be included. Additional options appear to specify the single gel lanes. **Note**: If you select both, "Electropherogram Single View" and "Gel Single View", the gel lane will be included immediately below the electropherogram and will share the axis with the electropherogam. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
Scale Type of Axis	If you select "Size" (in DNA and RNA mode), or "Molecular Mass" (in protein mode), respectively, the axis will show a size scale based on the sample peaks, if the sample has been analyzed with a reference marker table and the alignment markers have been correctly identified. Otherwise, the axis will show relative migration time, if possible. If you select "Rel. Time", the axis will show relative migration time, if the sample has been analyzed and the alignment markers have been correctly identified. Otherwise, the axis will show an absolute time scale. If you select "Abs. Time [min]", the axis will show an absolute time scale. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
Zoom to Alignment Marker	Select this option, if available, to scale the lanes so that the lanes start with the lower alignment maker band and end with the upper alignment marker band (crop data outside of the alignment markers). **Note:** This is possible only if all samples are analyzed. **Note:** This option is not available if both, "Electropherogram Single View" and "Gel Single View", are selected.
Result Table	If you select this option, the result table will be included in the report. Additional options appear to configure the result table (see below).

Note: In RNA mode, if you want the 28 S/18 S ratio or the "RIS" to be included in the report, select the overview option "Peak Calling Result Table" (refer to Analysis of RNA samples for further information).

Note: In protein mode, if you want the absolute concentration to be included in the report, select the overview option "Peak Calling Result Table" (refer to Analysis of protein samples for further information).

Select the following optional information that you want to include in the result table:



"Result table" options in DNA mode.

Note: If the "Result Table option is selected, but no result table column is selected, the "Result Table" check box is marked yellow, and the report/export profile is invalid.

The result table options are described below.

Size	Adds the result table column "Size [bp]" or "Size [nt]" for DNA or RNA mode, respectively.
Molecular mass	For Protein mode only. Adds the result table column "m [kD]".
Concentration	For DNA and RNA mode only. Adds the result table column "Conc. [ng/µl]". If you select this option, the total concentration is added automatically as last value of the column.
Relative Concentration	For Protein mode only. Adds the result table column "Rel. Conc. [ng/µl]".
Molarity	For DNA and RNA mode only. Adds the result table column "Mol. [nmol/l]".
Height Percentage	Adds the result table column "Height %".
Normalized Area	Adds the result table column "NA".
Normalized Area Percentage	Adds the result table column "NA %".
Signal to Noise	Adds the result table column "S/N" (Signal-to-noise ratio).
FWHM	Adds the result table column "FWHM [sec]" (full width at half maximum).
Resolution	Adds the result table column "Res.".
Ratio Normalized Area	Adds the result table column "Ratio NA".
Time	Adds the result table column "Time".
Rel.Time	Adds the result table column "Rel. Time".
Start	Adds the result table column "Start".
Stop	Adds the result table column "Stop".
Height	Adds the result table column "Height".
Area	Adds the result table column "Area".

Note: Refer to section Peak result columns for more information about the columns.

Note: You can specify the field order of the result table in the report by drag-and-drop. Left-click on a column name and drag it to the new position.

6.4.11.3 Exporting data

The basic procedure of exporting data in the "Analysis" environment is as follows:

1. Load the samples using the "Experiment Explorer".
   For more details about loading sample data, see section Loading sample data.
2. Inspect the samples before exporting.
   See the Viewing sample data section for more details on data inspection.
   For this step the "Gel view" or the "Electropherogram overview" are especially useful.

3. Select the samples you want to export.
   For more details about selecting samples, see section Selecting samples for analysis or report
4. Select export settings and start exporting.

   On the right side of the analysis environment, the report toolbar can be found.

   If it is not visible, you can display it using the "View" menu (selecting the menu item "View"/"Show Analysis Parameters") or by clicking the icon at the extreme right of the view selection bar:

   Select the "Report" tab of the toolbar.

   Select a predefined report/export profile. The export settings of the selected profile are shown below the report settings. For details refer to the Export options section.

   Make sure that at least one of the export options is selected. If not, select another predefined report/export profile. (Users assigned the user roles "Advanced User" or "Basic User" may modify the settings as they wish.)

   Specify the directory to which the export files will be saved to (refer to section Export options for information about how to specify the export directory).

   Click the "Start Report/Export" at the bottom of the "Report" tab to start exporting.

   Note: The button "Start Report/Export" is disabled if no samples are selected in the view (see Step 3).

   The export files will be generated automatically and stored in the specified directory.

6.4.11.4 Export options

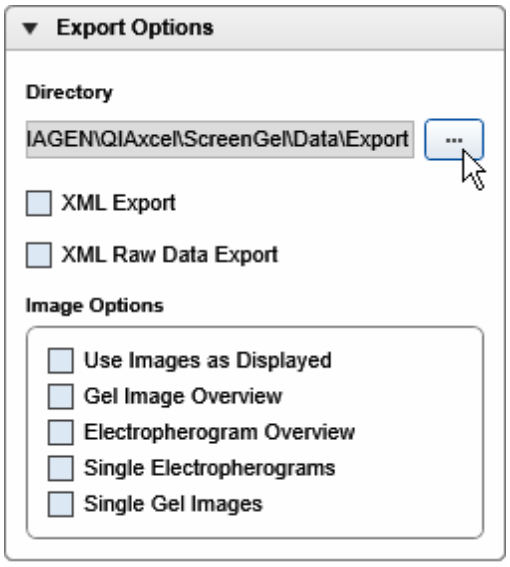
The report/export settings are divided into two groups:

- "Report Options" containing the report settings
- "Export Options" containing the export settings

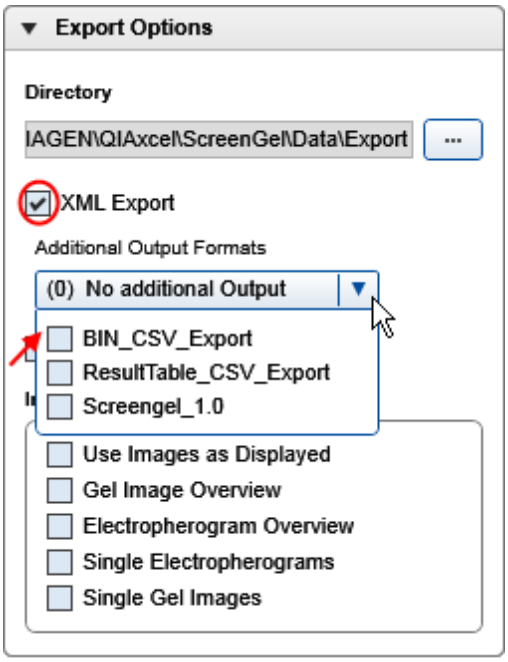
Note: You can collapse and expand each group by clicking ▼ and ▶ to the left of the group name.

Collapse the report options or scroll down to see the export options.

"Export Options"



"Export Options".



Additional output formats.

The options are described below.

Directory	Select the directory to which the export files will be saved by clicking . In the dialog box that appears, navigate to the correct directory and click "OK".
XML Export	If you select this option, an export file in XML format will be generated. This file contains all general experiment and sample details of the selected samples, except electropherogram raw data. If the samples are analyzed, it contains the analysis results. An additional option to select additional output formats appears. The software provides two formats. You can select all of them.

BIN_CSV_Export	Use this option to export the peak calling result table in .csv format (similar to the file format that was exported by the "BioCalculator 3.2" software).
ResultTable_csv_table	Use this option to export the analysis results in .csv format (similar to the file format that was exported by the "BioCalculator 3.2" software).
ScreenGel_1.0	Use this option to convert the export file to the xml export format of the QIAxcel ScreenGel software version 1.0.

Note: You can customize your own output formats. Define xslt scripts based on the xml export file and store them in the %DATA_DIR% \ReportExportProfile\XSLT_Export directory. Script processing (e.g., VB- or Java-Script) within a XSLT style sheet is supported. In XSLT style sheets, the configured export directory is available as the parameter "exportPath".

XML Raw Data Export	If you select this option, electropherogram raw data of the selected files will be exported in XML format. An additional option to select additional output formats appears. The software provides one format.

RawData_CSV_Export	Use this option to export the electropherogram raw data in .csv format (similar to the file format which was exported by the "BioCalculator 3.2" software).

Note: You can customize your own output formats. Define xslt scripts based on the xml raw data export file and store them in the <%DATA_DIR% >\ReportExportProfile\XSLT_RawExport directory. Script processing (e.g., VB- or Java-Script) within a XSLT style sheet is supported. In XSLT style sheets, the configured export directory is available as the parameter "exportPath".

The image options are described below.

Use Images as Displayed	Use this option to obtain images that look similar to the presentation in the QIAxcel ScreenGel software regarding alignment, scales, labels, zoom, etc. **Note:** This option is available in the analysis environment only, it may not be used in a process profile.

Gel Image Overview

Use this option to export the gel image of all selected samples.

Note: The gel image in the export will have the left-hand y-axis on both sides, also if the "Use Images as Displayed" option is selected.

Additional options appear to specify the gel layout.

Scale Type of Y-axis

If you select "Size" (in DNA and RNA mode) or "Molecular Mass" (in protein mode), respectively, the y-axis will show a size scale based on the reference marker on both sides of the gel image, also if the "Use Images as Displayed" option is selected. The lanes in the gel image will be aligned according to the alignment markers.

Note: The size scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed with the same reference marker table, and the alignment markers have been correctly identified. Otherwise, the y-axis will show relative migration time, if possible.

If you select "Rel. Time", the y-axis will show relative migration time. The lanes in the gel image will be aligned according to the alignment markers.

Note: The relative time scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the lanes cannot not be aligned and the y-axis will show an absolute time scale.

If you select "Abs. Time [min]", the lanes will not be aligned and the y-axis will show an absolute time scale.

Note: This option is not available if the "Use Images as Displayed" option is selected.

Zoom to Alignment Marker

Select this option to scale the lanes, so that the lanes start with the lower alignment maker band, and end with the upper alignment marker band, if available (crop data outside of the alignment markers).

Note: This is possible only if all samples are analyzed.

Note: This option is not available if the "Use Images as Displayed" option is selected.

Standard layout

Specify the number of lanes per row: 4, 6, 8, 12, 16, 24, 32, 36, or 48. The lanes are printed from left to right as shown by the first layout pictogram. The lane order is the same as in the view. The lanes are labeled with sample position, sample information, plate ID, run number, and entry number.

	Use this option if you intentionally changed the lane order.
Horizontal plate layout	The lane order is fixed according to the positions of a plate, starting with A1 at the upper left and ending with H12 at the lower right. Positions for samples not selected remain empty. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
Vertical plate layout	The lane order is fixed, starting with H1 at the upper left and ending with A12 at the lower right. Positions for samples not selected remain empty. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
Reverse vertical plate layout	The lane order is fixed, starting with A1 at the upper left and ending with H12 at the lower right. Positions for samples not selected remain empty **Note:** This option is not available if the "Use Images as Displayed" option is selected.

	Split plate layout	The lane order is fixed. The vertical plate layout is split as shown in the last pictogram. Positions for samples not selected remain empty. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
	Rows per file	Use this option to specify the number of rows to be included in one file (the image is split into several files after the specified number of rows). **Note:** This option is not available if the "Standard layout" option is selected. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
	Individual Scaling	Select this option to auto-scale the contrast for each gel lane individually. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
Electropherogram Overview	Select this option to export the electropherogram overview for all selected samples. The order is the same as in the view. Additional options appear to specify the electropherogram overview. If a sample is analyzed, all detected peaks are marked (red apex, green apex for alignment markers).	
	Scale Type of X-axis	If you select "Size" (in DNA and RNA mode) or "Molecular Mass" (in protein mode), respectively, the x-axis will show a size scale based on the reference marker. The electropherograms will be aligned according to the alignment markers. **Note**: The size scale can be created only, if all selected samples have been run with the same alignment marker, have been analyzed with the same reference marker table, and the alignment markers have been correctly identified. Otherwise, the x-axis will show relative migration time, if possible. If you select "Rel. Time", the x-axis will show relative migration time. The electropherograms will be aligned according to the alignment markers. **Note**: The relative time scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the electropherograms will not be aligned and the x-axis will show an absolute time scale. If you select "Abs. Time [min]", the electropherograms will not be aligned and the x-axis will show an absolute time scale.

		Note: This option is not available if the "Use Images as Displayed" option is selected.
	Zoom to Alignment Marker	Select this option, if available, to scale the electropherograms so that the electropherograms start with the lower alignment maker peak, and end with the upper alignment marker peak (crop data outside of the alignment markers). **Note:** This is possible only if all samples are analyzed. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
	Individual Scaling	Select this option to auto-scale the y-axis for each electropherogram individually. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
	Electropherograms per page	For the "Electropherogram Overview" specify the number of electropherograms per file.
Single Electropherograms	Select this option to export the electropherograms for all selected samples in separate files. If the sample has been analyzed, baseline, threshold line, and peak markers (start, stop, red apex, green apex for alignment markers) are included. Additionally, peak labels are included showing the peak size, if determined, otherwise, the relative migration time is shown. Use the "Use Images as Displayed" option to export the electropherogram as displayed. Additional options appear to specify the single electropherograms. **Note:** If the "Use Images as Displayed" option is selected, the gel lane is combined with the electropherogram if it is visible in the QIAxcel ScreenGel software.	
	Scale Type of X-axis	If you select "Size" (in DNA and RNA mode) or "Molecular Mass" (in protein mode), respectively, the x-axis will show a size scale based on the reference marker, if the sample has been analyzed with a reference marker table and the alignment markers have been correctly identified. Otherwise, the x-axis will show relative migration time, if possible. If you select "Rel. Time", the x-axis will show relative migration time, if the sample has been analyzed and the alignment markers have been correctly identified. Otherwise, the x-axis will show an absolute time scale. If you select "Abs. Time [min]", the x-axis will show an absolute time scale. **Note:** This option is not available if the "Use Images as Displayed" option is selected.

Zoom to Alignment Marker	Select this option to scale the electropherograms, so that the electropherograms start with the lower alignment maker peak, and end with the upper alignment marker peak, if available (crop data outside of the alignment markers). **Note:** This is possible only if all samples are analyzed. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
Individual Scaling	Select this option to auto-scale the y-axis for each electropherogram individually. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
Display Gel Image below Electropherogram	Select this option to export the gel lane combined with the electropherogram (the gel lane is below the electropherogram). Note: This option is not available if the "Use Images as Displayed" option is selected.
Electropherograms per page	For the "Electropherogram Overview" specify the number of electropherograms per file.

Single Gel Images	Use this option to export the gel lanes for all selected samples individually. Additional options appear. **Note:** This option is not available if the "Use Images as Displayed" option is selected.

Scale Type of Axis	If you select "Size" (in DNA and RNA mode) or "Molecular Mass" (in protein mode), respectively, the axis shows a size scale based on the sample peaks, if the sample has been analyzed with a reference marker table and the alignment markers have been correctly identified. Otherwise, the axis will show relative migration time, if possible. If you select "Rel. Time", the axis will show relative migration time, if the sample has been analyzed and the alignment markers have been correctly identified. Otherwise, the axis will show an absolute time scale. If you select "Abs. Time [min]", the axis will show an absolute time scale. **Note:** This option is not available if the "Use Images as Displayed" option is selected.
Zoom to Alignment Marker	Select this option, if available, to scale the lanes so that the lanes start with the lower alignment maker band, and end with the upper alignment marker band (crop data outside of the alignment markers). **Note:** This is possible only if all samples are analyzed.

The image export settings are described below. They appear if at least one image type is selected for export.

File Type	Select the file type for the image files.
Resolution	Select the resolution for the image files; the available resolutions are: 75 dpi (dots per inch), 150 dpi, 300 dpi, and 600 dpi. For small bands, use 150 dpi.

6.4.11.5 Modifying a report/export profile

Note: Only users with the "Advanced User" or "Basic User" role can modify report/export options.

To modify a report/export profile proceed as follows:

1. Open the "Report" tab.

   If it is not visible, you can display it using the "View" menu (selecting the menu item "View"/"Show Analysis Parameters") or by clicking the icon at the extreme right of the view selection bar:

Select the "Report" tab.

2. Select the report/export profile you want to modify.

   Select the report/export profile in the "Report/Export Profile" drop-down list.

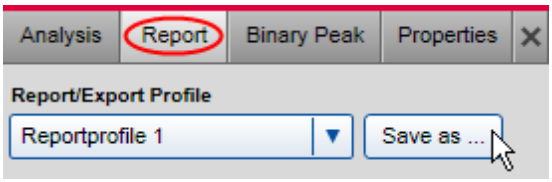
3. Change the profile options according to your needs.

   See the Report options and Export options sections for detailed information.

   Note: The system notifies modifications on the profile by displaying a "*" at the beginning of the profile name.

4. Save the modified report/export profile.

   Click the "Save as ..." button. Click "OK" in the "Save Profile" dialog box which appears.



Saving a report/export profile.

Note: If you want to use the modified report/export options only once, just click "Start Report/Export" without saving the modifications. However, your changes will lost when you select another report/ export profile.

Note: Report profiles provided by QIAGEN cannot be modified. However, to save your modifications enter a new unique profile name in the "Save Profile" dialog box. A new profile will be created containing your modifications. This is possible for users with the "Advanced User" role only.

6.4.11.6 Creating a new report/export profile

Note: Only users with the "Advanced User" role can create a new report/export profile.

To create a new report/export profile proceed as follows:

1. Open the "Report" tab.

   If it is not visible, you can display it using the "View" menu (selecting the menu item "View"/"Show Analysis Parameters") or by clicking the icon at the extreme right of the view selection bar:

   Select the "Report" tab.

2. Select a report/export profile.

   Select the profile from the "Report/Export Profile" drop-down list. The selected profile serves as a template for the creation of the new profile.

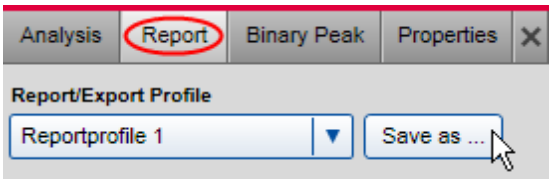
   Note: Select "NewReport/ExportProfile" to create a report/export profile from scratch. The system will show "*NewReport/ExportProfile" after selection.

3. Set the profile options according to your needs. See the Report options and Export options section for detailed information about report/export options.

Note: The system notifies modifications on the profile by displaying a "*" at the beginning of the profile name.

4. Save the modified report/export profile under a new name.

   Click the "Save as ..." button and enter a new unique profile name in the "Save Profile" dialog box that appears.

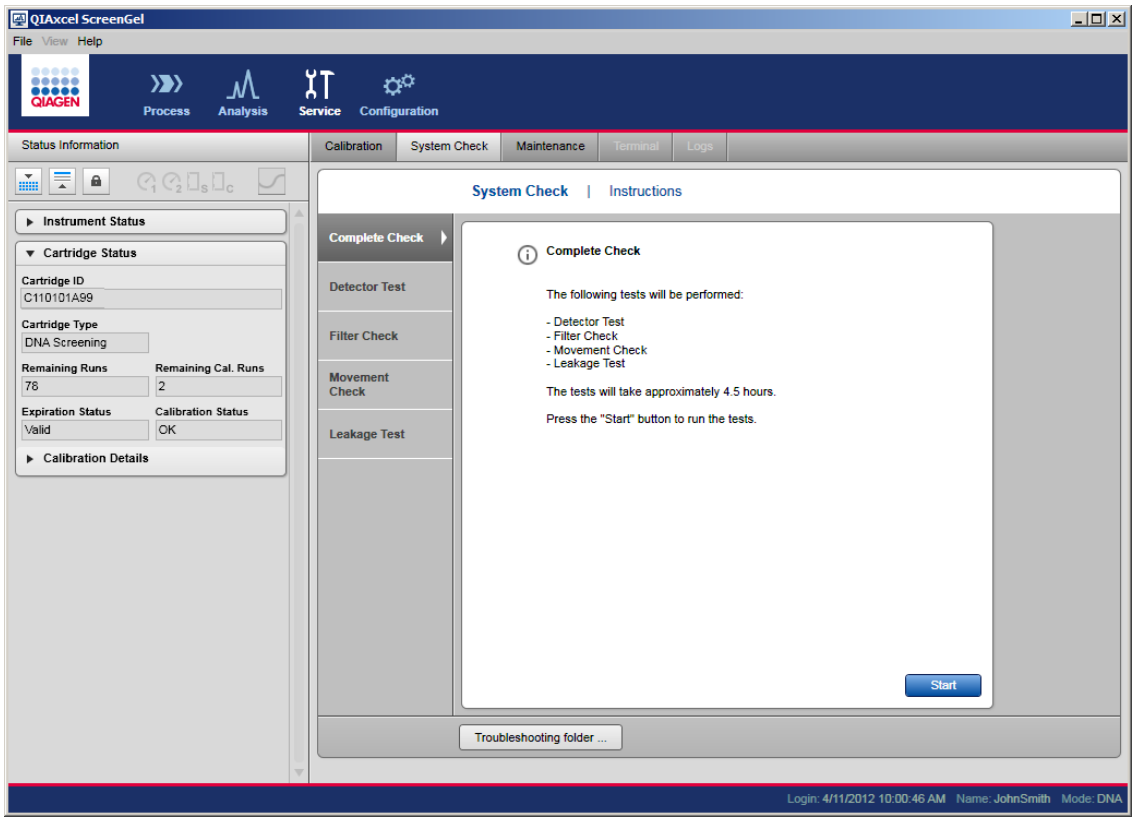


Saving a report/export profile.

6.5 Service

The "Service" environment provides functionality for cartridge calibration as well as troubleshooting and maintenance tools for the QIAxcel Advanced instrument.

On the left side of the service environment, a "Status Information" panel is displayed (See "Status Information" panel).



"Service" environment with active "System Check" screen. The "Status Information" panel is shown to the left of the screen.

Note: The "Terminal" and "Logs" screens of the "Service" environment may be accessed by service personnel only and are not described in this manual.

6.5.1 Calibrating a cartridge

Every new cartridge requires intensity calibration prior to sample analysis. The intensities of each capillary are normalized and a factor is applied for every subsequent run. This corrects for natural intensity reading variations between each capillary in the cartridge. The data for each cartridge intensity calibration are stored in a single file named **<cartridge-id>_<instrument-id>.xcc**. This file is saved in the directory **%DATA_DIR%\CartridgeCalibrationData**.

Note: To inspect calibration data, switch to the analysis environment and click the "Load experiment" button of the experiment explorer. In the file dialog that appears, select the path ending with "[Calibration results]".

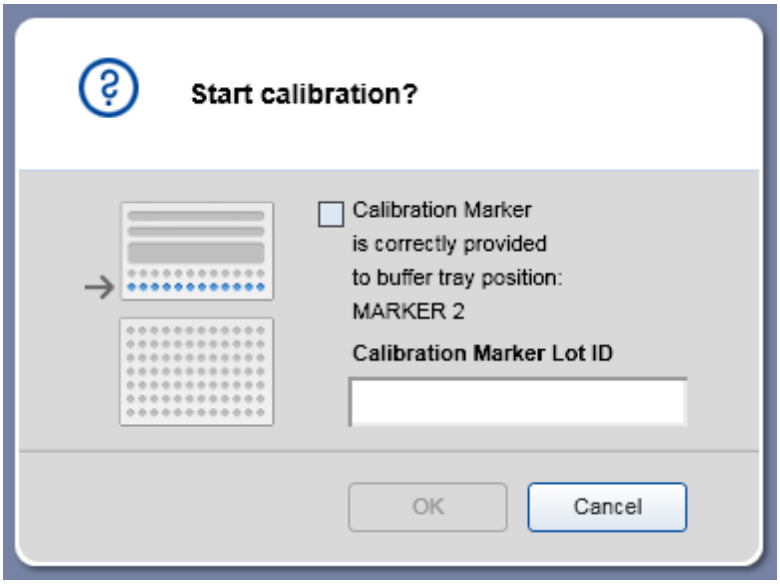
Note: If for any reason a different computer is used to the one containing the calibration file, the file should be transferred to the new computer. Otherwise, recalibration of the cartridge is required.

6.5.1.1 Running the calibration wizard

Intensity calibration of the cartridge is performed in the "Calibration" screen of the "Service" environment:

1. Load QX Intensity Calibration Marker onto the buffer tray position MARKER2 as detailed in Preparing the buffer tray step 7.
2. Launch the calibration run by clicking the "Start calibration" button.

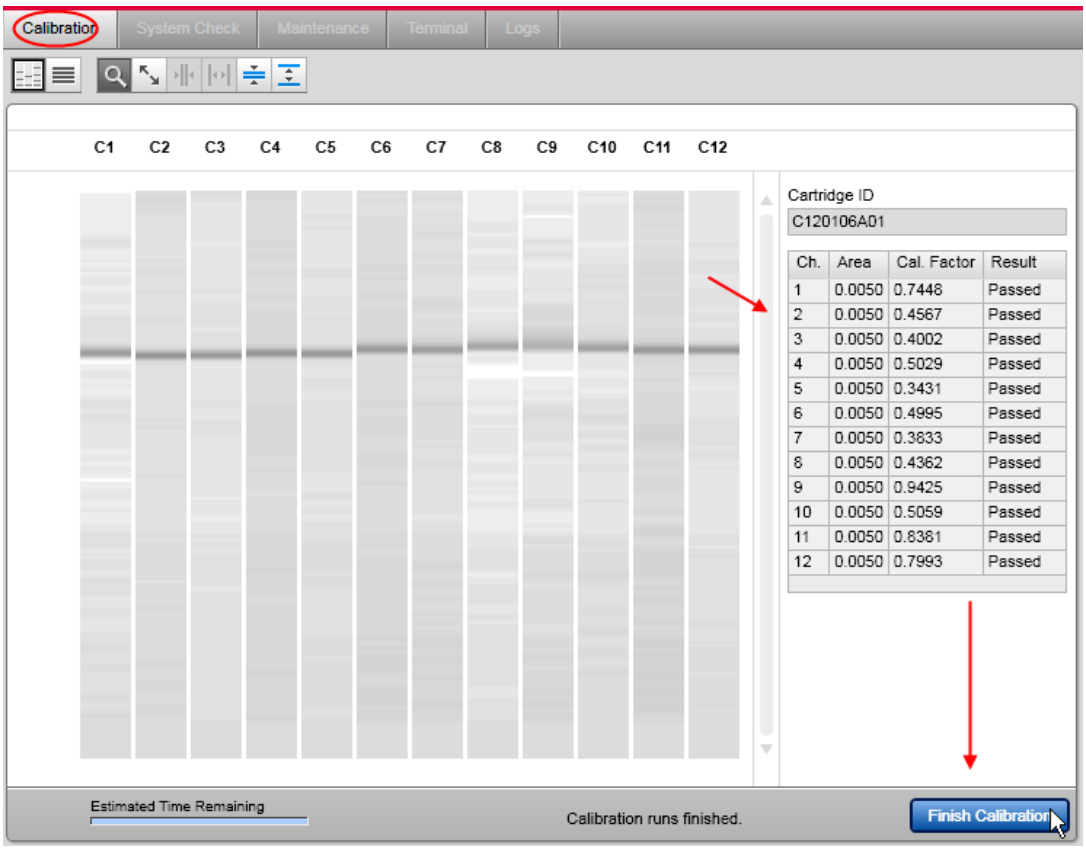
   Note: The total run time for the calibration routine is about 16 minutes.
3. Confirm that the QX Intensity Calibration marker is loaded. Optionally, enter the lot ID. Start the calibration by clicking the "OK" button.



Confirmation dialog

If the QX Intensity Calibration Marker is not loaded correctly, cancel the dialog. Load it again and repeat step 1.

4. Once the calibration is complete, the calibration results are displayed next to the gel/ electropherogram view. The result table shows the area, calibration factor, and the result ("Passed" or "Failed") for each channel.



Calibration results.

Note: A successfully calibrated cartridge should have a normalized area in a range as described in the respective kit handbooks.

Note: If one or more channels fail, the calibration process should be repeated. If the issue persists, please contact QIAGEN Technical Services or refer to the "troubleshooting" section in the handbook supplied with the QIAxcel Kit you are using.

5. Accept the calibration result. The cartridge is now calibrated.

   Note: Discard the calibration result if one or more channels fail.

   Note: A user with user role "Advanced user" can accept calibration results even if one ore more channels failed. In this case the calibration status will be "Conditional OK". Only users with the user role "Advanced User" can perform processes using cartridges with calibration status "Conditional OK".

6.5.1.2 Recalibrating a cartridge

To recalibrate a cartridge, repeat the procedure detailed in Running the calibration wizard. The calibration results of previous calibration procedures are discarded when recalibrating a cartridge.

Note: It is possible to calibrate a cartridge that has no calibration runs left. In this case, three regular runs are used instead of one calibration run.

6.5.2 System Check

The "System Check" screen of the "Service" environment provides several procedures for detecting problems with the QIAxcel Advanced instrument:

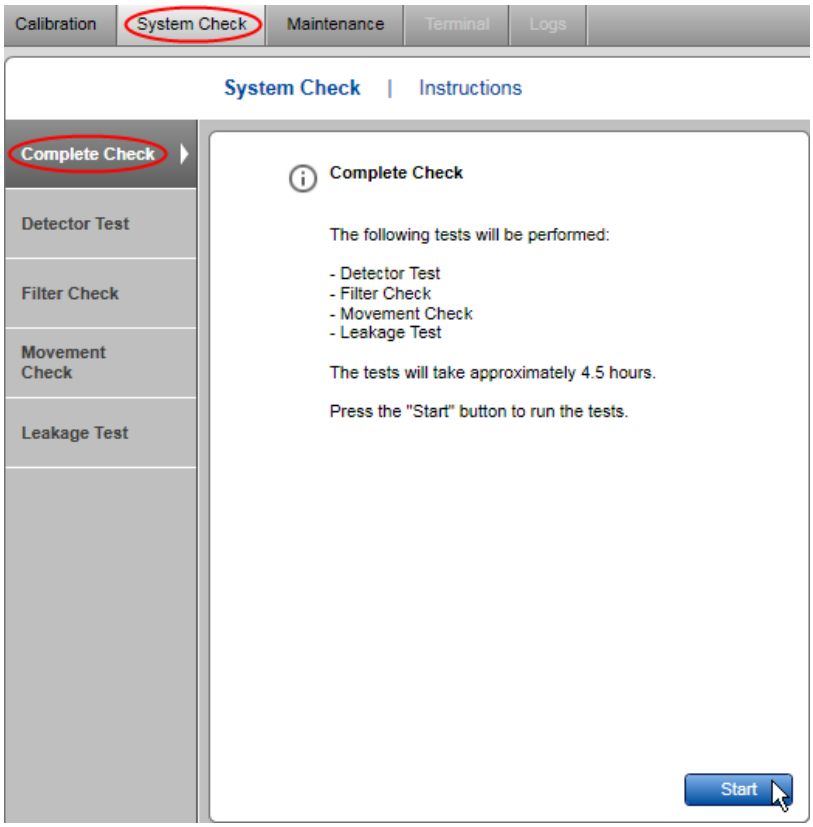
- Complete Check
  The complete check performs all the system checks listed below.
- Detector Test
  The detector test checks the raw count of all 12 channels.
- Filter Check
  The filter check detects blockage of the purge filter.
- Movement Check
  The movement test verifies that the sample tray can be moved properly and that the position sensors work as expected.
- Leakage Test
  The leakage test checks for N2 leakage.

Note: The test results are stored to the directory **%DATA_DIR%\SystemTest**.

Note: The troubleshooting folder functionality is described in the Troubleshooting folder section.

6.5.2.1 Complete Check

A "Complete Check" performs all available system checks: Detector Test, Filter Check, Movement Check and Leakage Test.



Complete check.

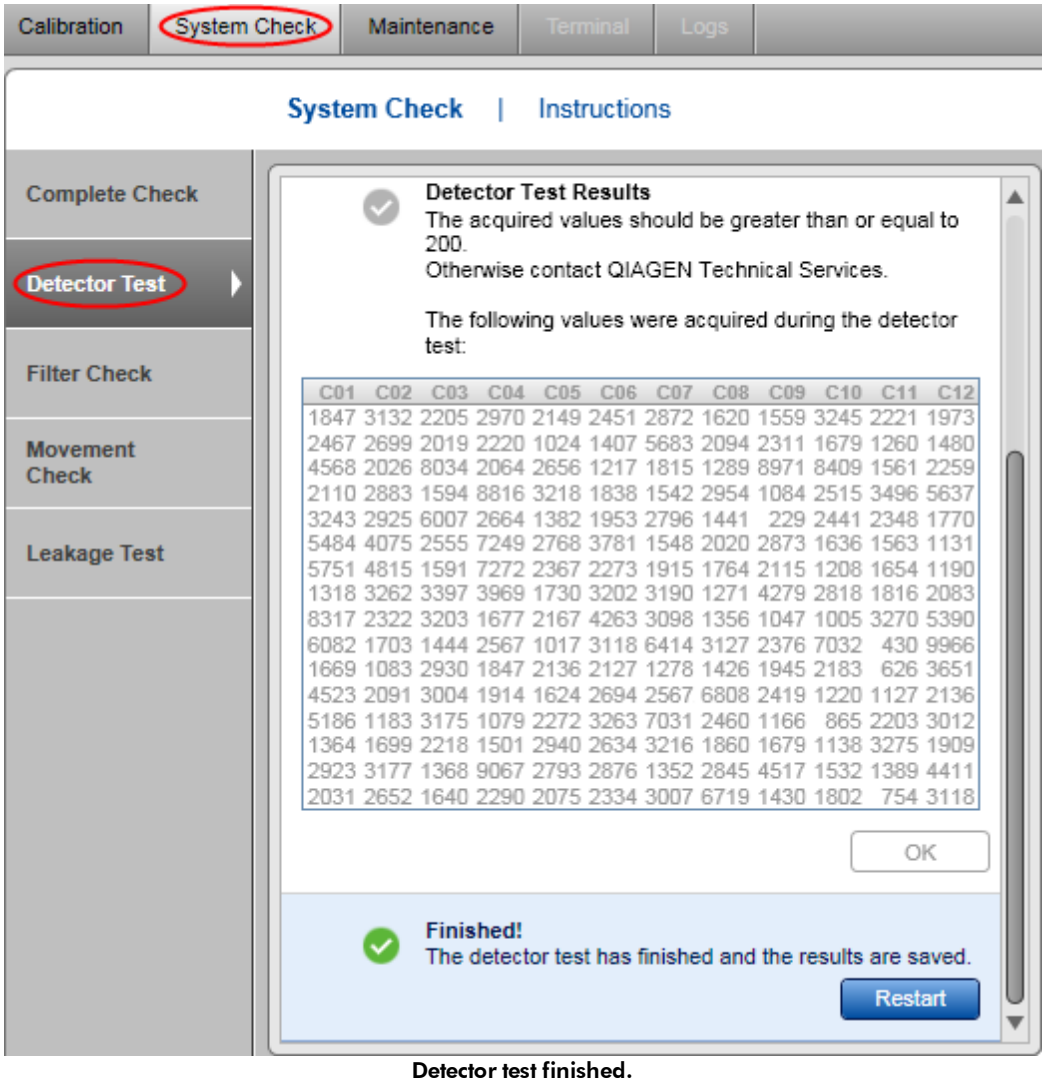
Note: The complete check takes approximately 4.5 hours.

6.5.2.2 Detector Test

The "Detector Test" verifies that the detectors of all 12 channels of the QIAxcel Advanced instrument work as expected. It may be performed when one or more channels in a new cartridge do not provide data signals and the baseline is flat.

Perform the "Detector Test" by following the instructions shown on the screen. The test takes only several seconds. At the end of the test, the acquired data is shown, and the results are stored.

Note: If not instructed otherwise, perform this test with a cartridge inserted and latched.



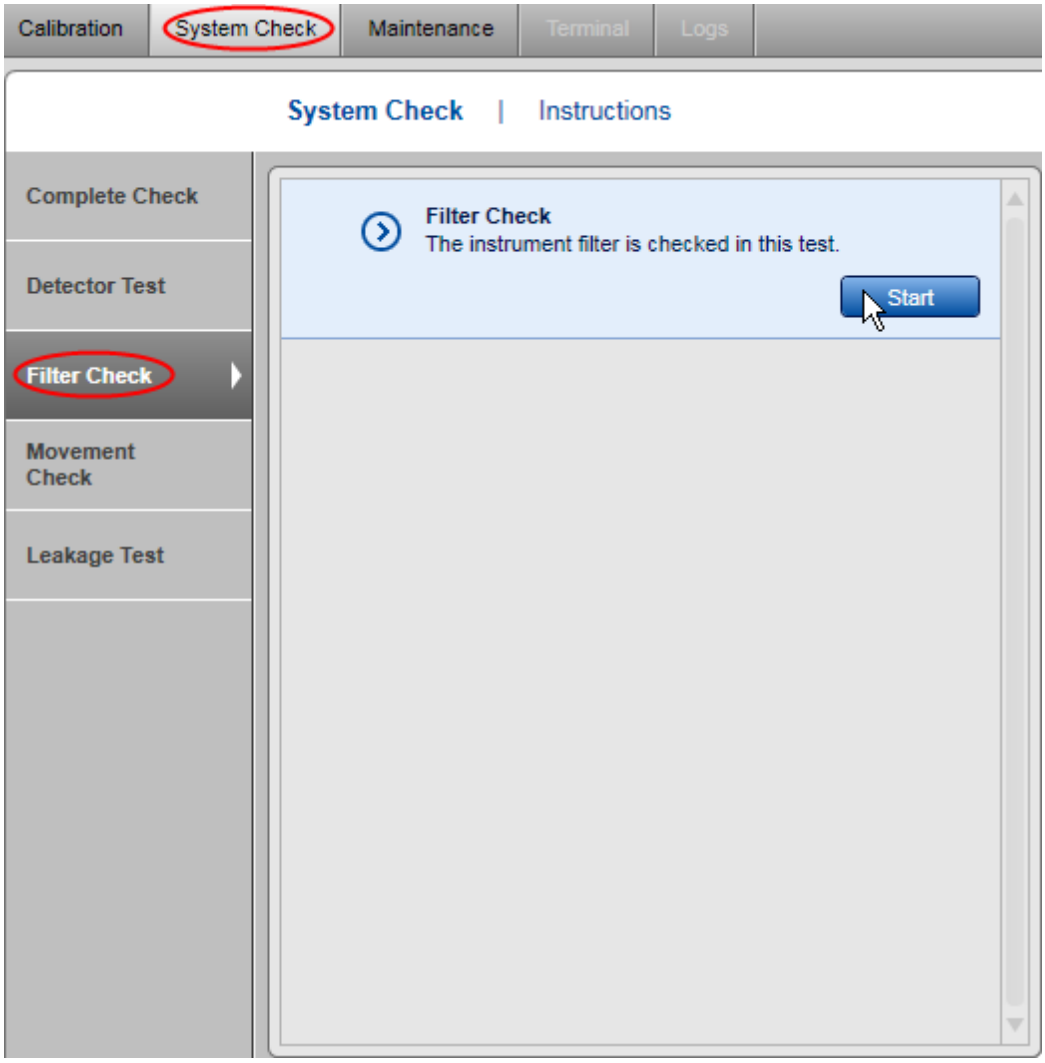
Detector test finished.

6.5.2.3 Filter Check

In rare instances, the purge filter that sits inside the QIAxcel Advanced instrument may become blocked with gel carryover. This blockage can be diagnosed using the "Filter Check". It takes about two minutes. At the end of the check, the filter status (passes or failed) is shown and the results are stored.

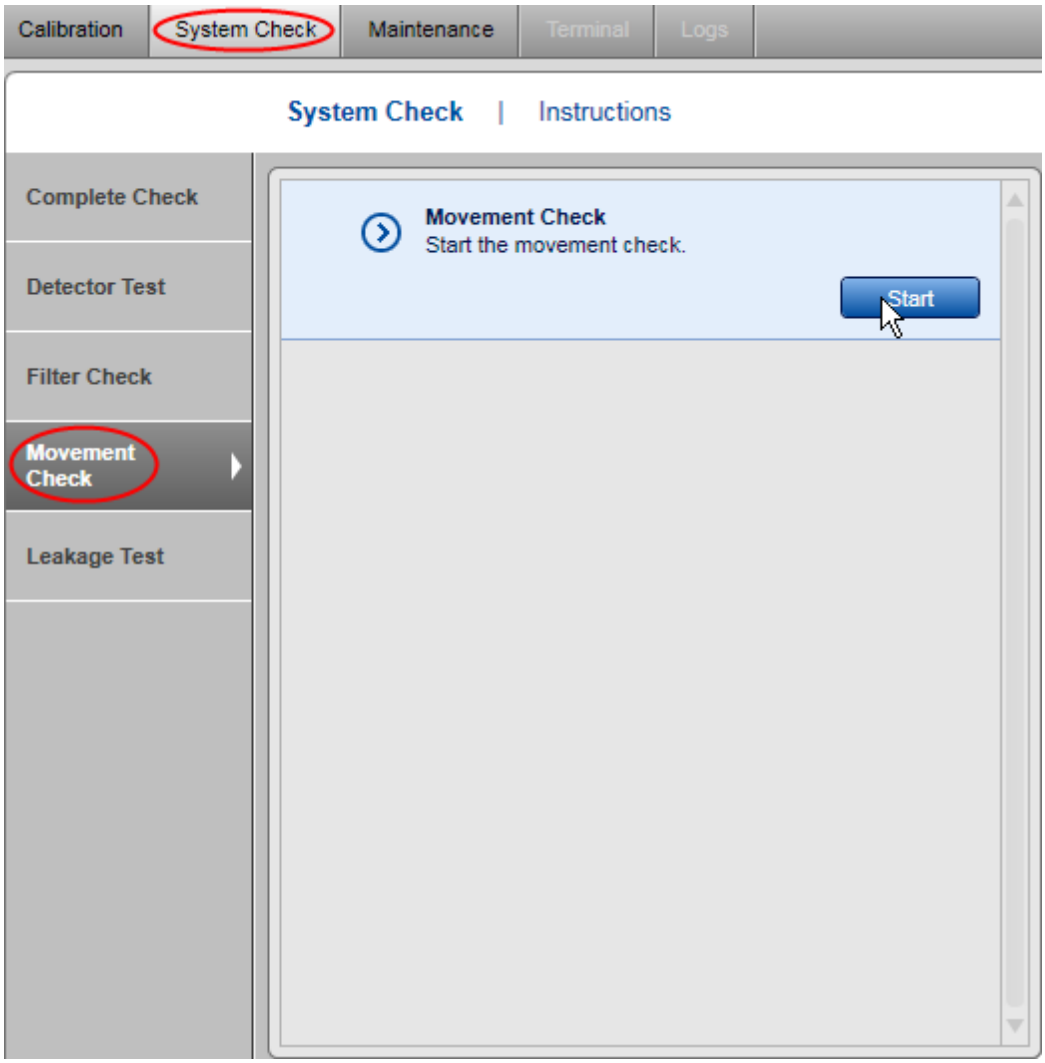
Note: A cleaning tissue, for example Kimwipe, is needed for this check.

The "Filter Check" is performed by following the instructions shown in the wizard:



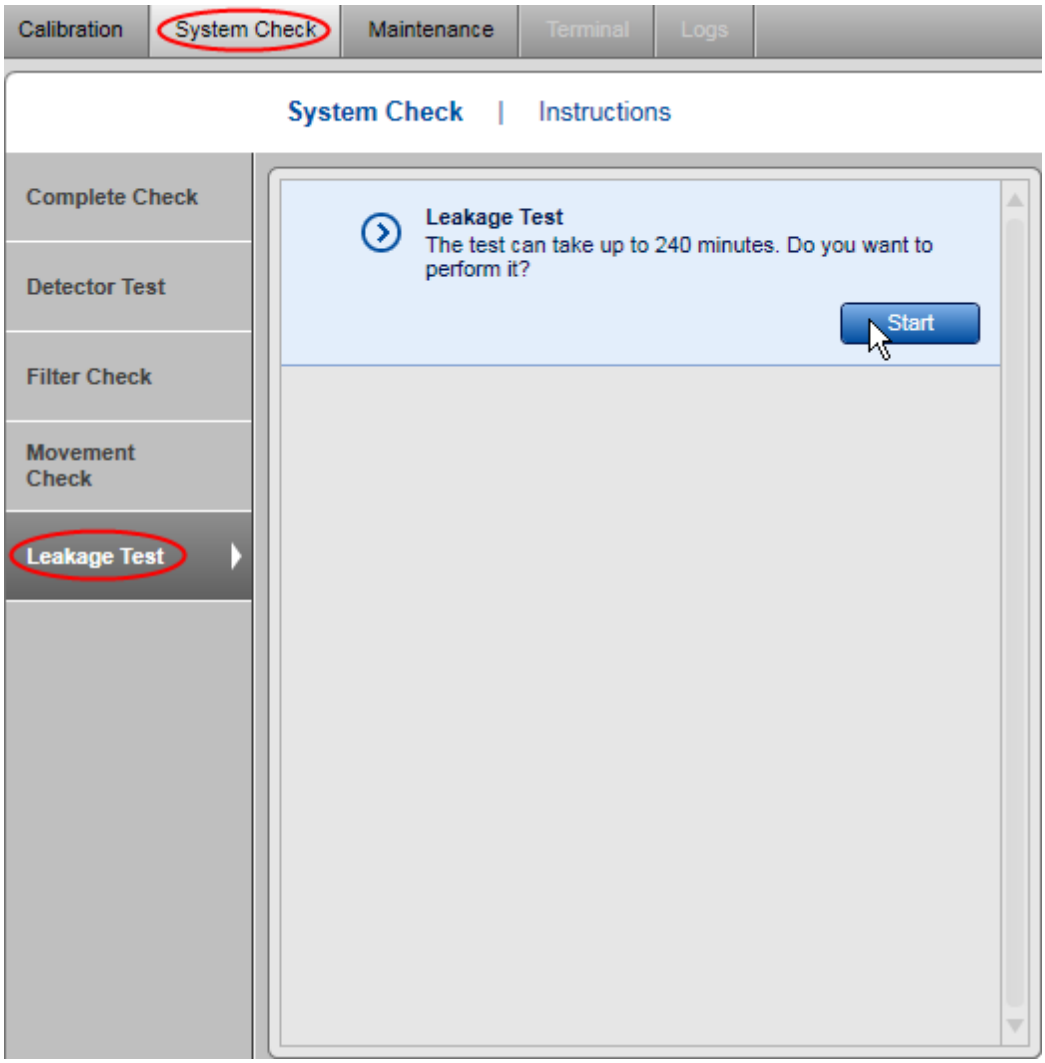
6.5.2.4 Movement Check

The "Movement Check" verifies that the tray motors and tray sensors work as expected. This test is fully automated and requires no user interaction except cartridge removing. It takes several seconds. At the end of the test, a test summary (passed or failed) is shown and the results are stored.



6.5.2.5 Leakage Test

The "Leakage Test" checks for leakages in the N_2 tubing of the QIAxcel Advanced instrument. This fully automated test takes approximately 240 minutes. After the test, the leakage rate is calculated if a leakage is detected and the results of the test are stored.



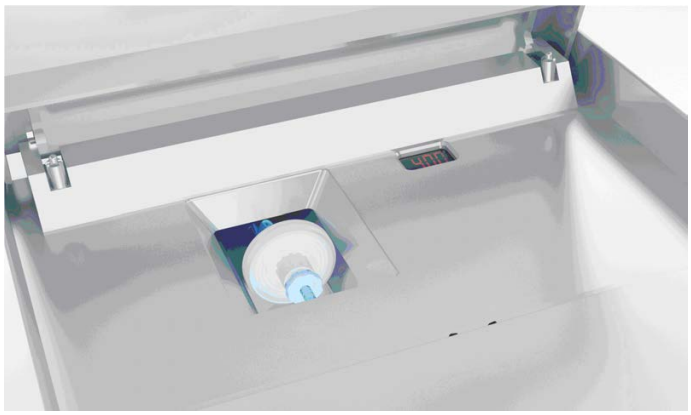
6.5.3 Maintenance

The maintenance screen of the "Service" environment provides several maintenance and troubleshooting procedures for the QIAxcel Advanced instrument and cartridges:

- Motor Teaching (for service personnel only; not described here)
- Purge
- Long Purge
- Empty N_2 Bottle
- Set Instrument ID
- Troubleshooting folder

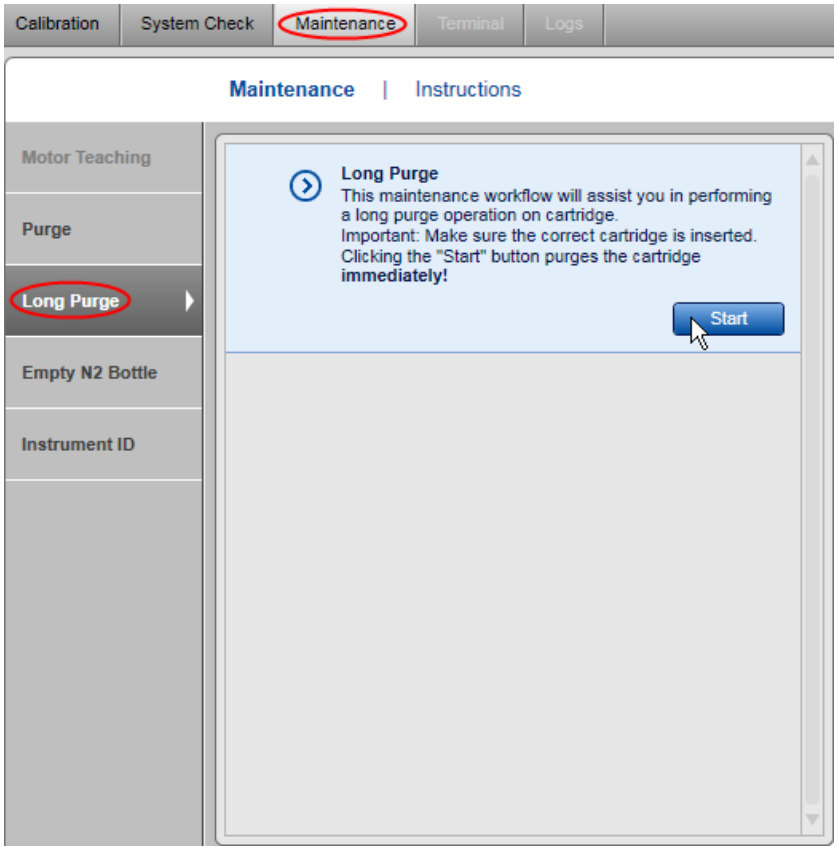
6.5.3.1 Purge

The "Purge" method allows the user to remove air bubbles from the gel cartridge and clean the capillaries. The process is fully automated and takes less than a minute.



6.5.3.2 Long purge

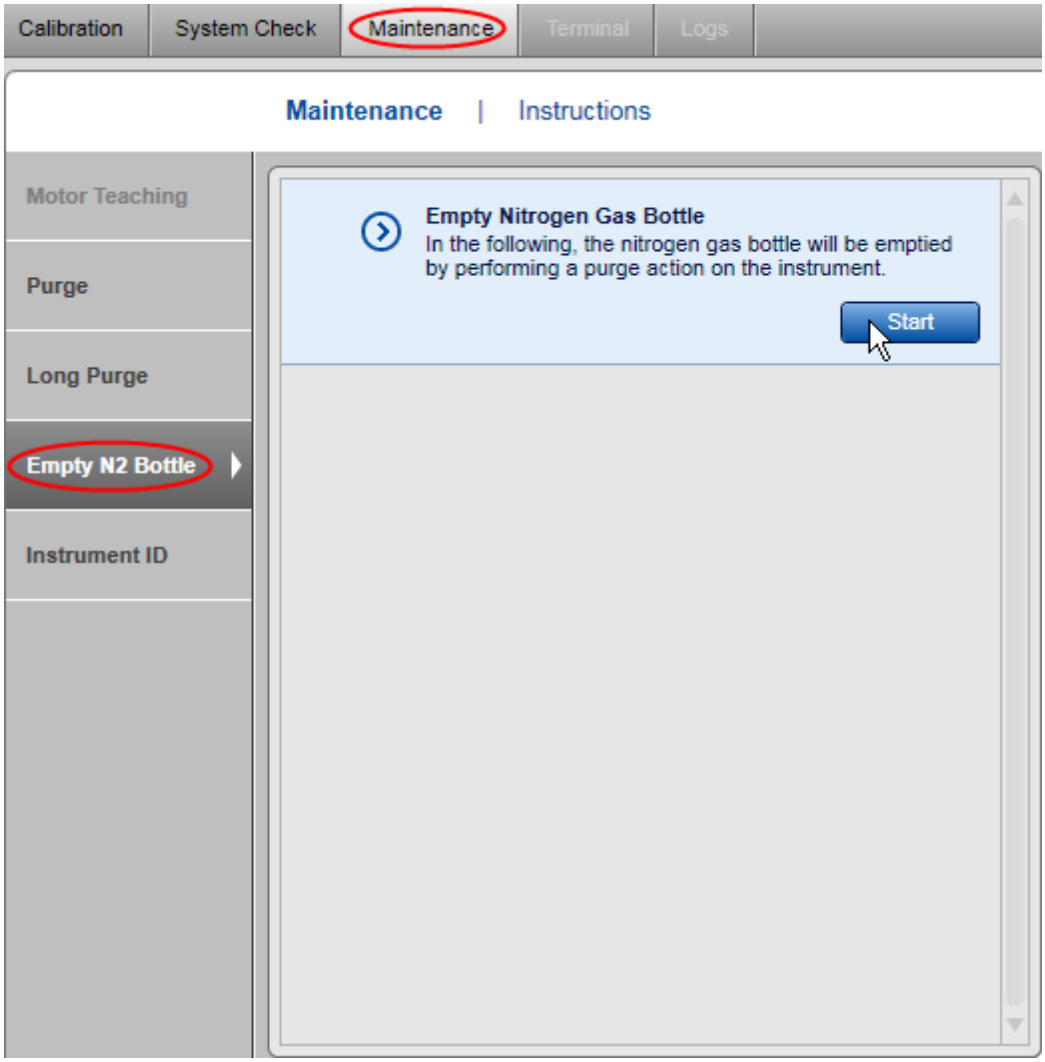
The "Long Purge" method allows the user to remove air bubbles from the gel cartridge and clean the capillaries extensively. The process is fully automated and takes about 3 minutes.



6.5.3.3 Empty N2 bottle

To remove a pressurized N_2 cylinder, you must release the remaining pressure first. The "Empty N_2 Bottle" function purges the nitrogen, which takes about a minute.

Note: You must first remove the QIAxcel gel cartridge before performing this action.



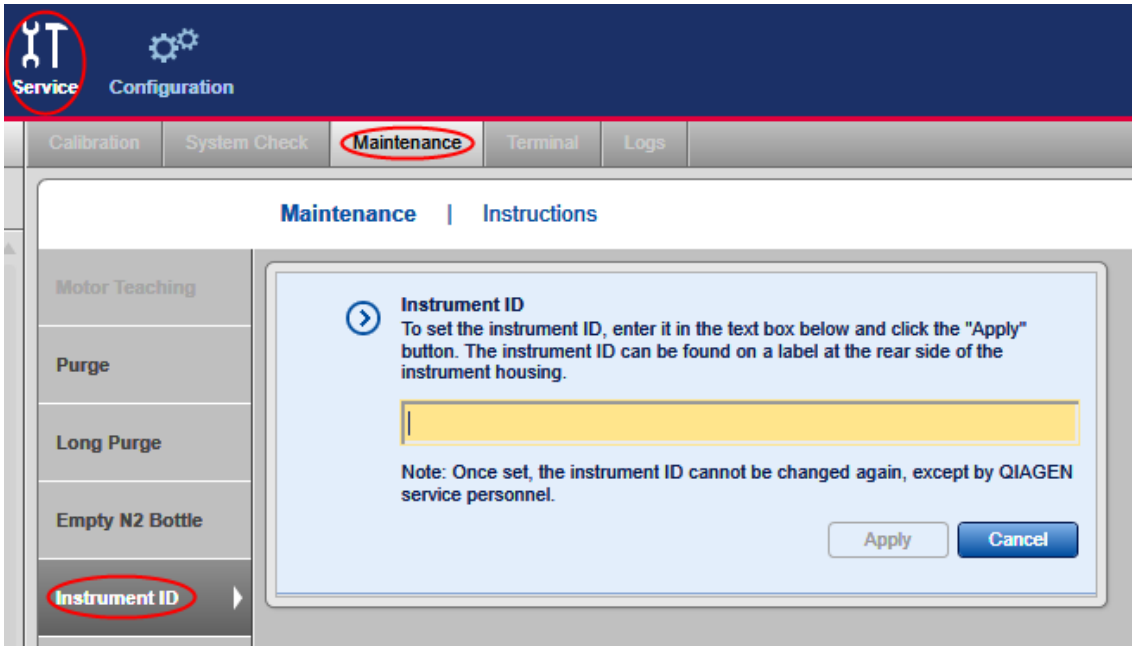
Important: Repeat this operation until no hissing sound can be heard at the end of the purge operation.

6.5.3.4 Setting the instrument ID

Setting the QIAxcel instrument ID (serial number) is possible only if the instrument is connected and the instrument ID has not been set. The instrument ID can be found on a label at the rear side of the instrument housing.

The instrument ID is required to identify each instrument and check that a cartridge is calibrated on a certain instrument (see Calibrating a cartridge).

Important: Make sure you have entered the correct instrument ID before clicking the "Apply" button. Once set, the instrument ID cannot be changed again, except by QIAGEN service personnel.

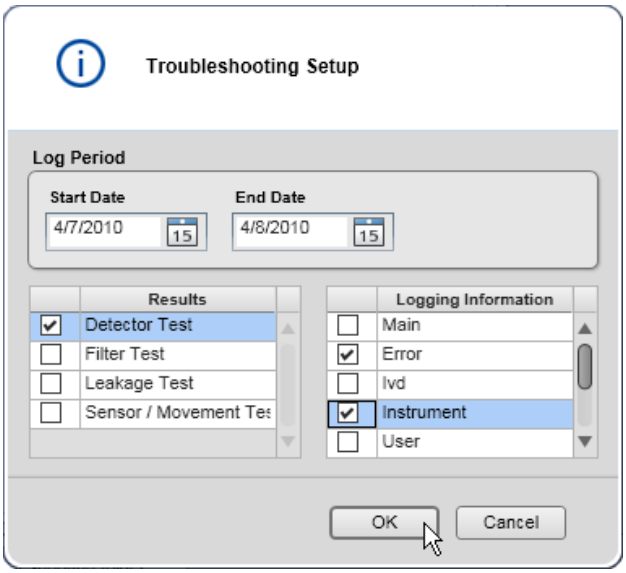

Service
Configuration
Calibration
System Check
Maintenance
Terminal
Logs
Maintenance | Instructions
Motor Teaching
Purge
Long Purge
Empty N2 Bottle
Instrument ID
Instrument ID
To set the instrument ID, enter it in the text box below and click the "Apply" button. The instrument ID can be found on a label at the rear side of the instrument housing.
Note: Once set, the instrument ID cannot be changed again, except by QIAGEN service personnel.
Apply
Cancel

6.5.3.5 Troubleshooting folder and log files

The "Troubleshooting folder" function allows export of log files and test results produced within a specified time period.

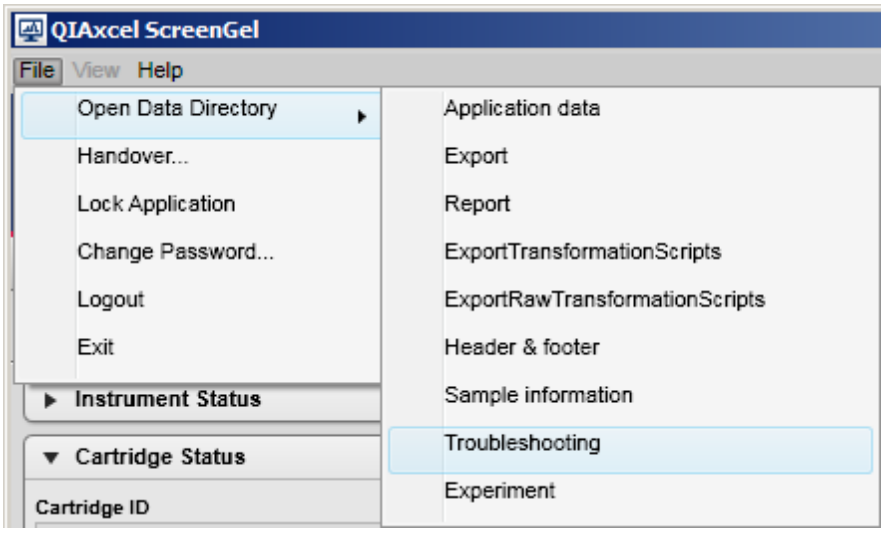
To export log files or test results, proceed as follows:

1. Switch to the "Service" environment.
2. Select the "Maintenance" or "System Check" screen.
3. Click the "Troubleshooting folder", which is located at the bottom of the screen. It opens the following dialog box:



Select information to be exported.

4. Select the time period in which the test results were produced or a problem occurred. In most cases, this is "Start Date": yesterday, and "End Date": today.
5. In the "Results" column, select the test results to be exported.
6. In the "Logging Information" column, select all log file types.
7. Click OK. The exported files are stored under the "Troubleshooting" directory defined in the Settings.
8. To navigate to the "Troubleshooting" directory, select the "Open Data Directory->Troubleshooting" option from the "File" menu .



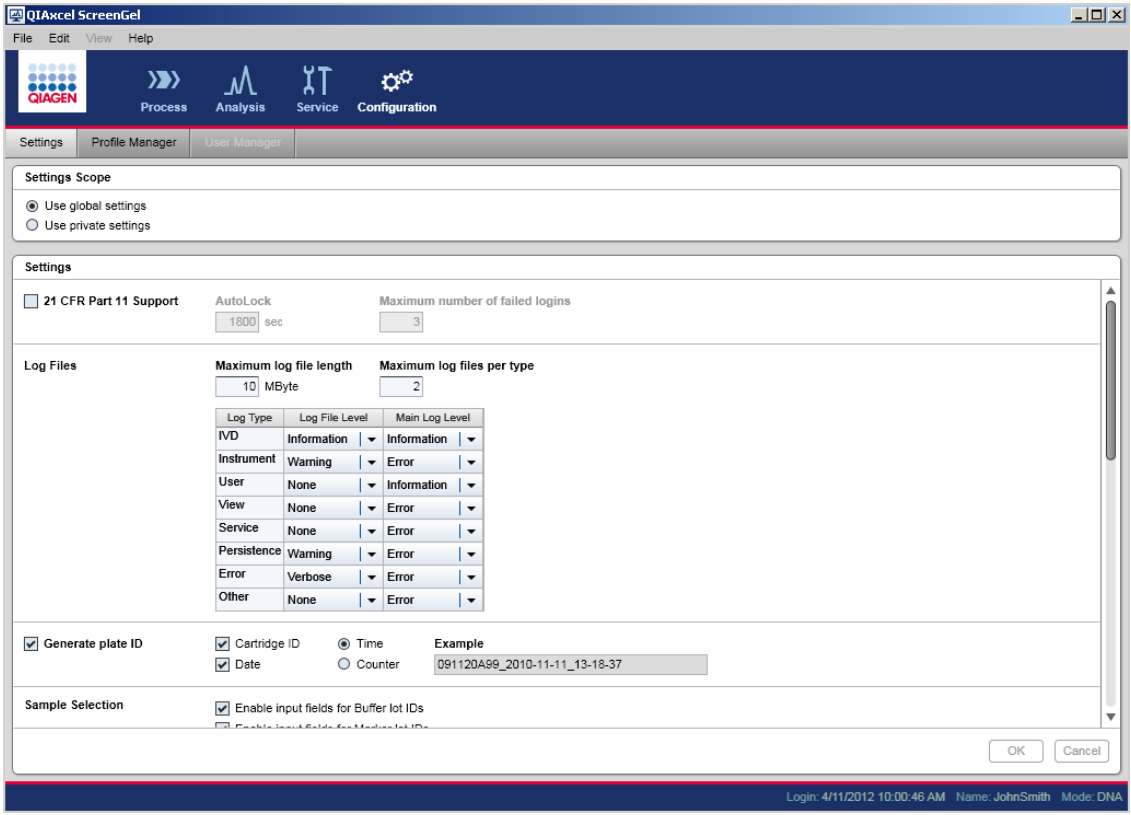
"Open Data Directory" function.

9. Select the just created file "Troubleshooting_..._.zip".

Refer to the Settings section for information about log file levels.

6.6 Configuration

Application settings, users, and profiles are managed in the "Configuration" environment:



"Configuration" environment with active "Settings" screen.

6.6.1 Settings

The "Configuration" environment of the QIAxcel ScreenGel software provides several settings options as described below.

Note: Global settings options are read only for users with the assigned role "Routine User" or "Basic User". Refer to the User roles section for more information.

Use global settings	The global settings option is used to share both general settings and profiles among several users.
Use private settings	When using private settings, both the general settings and the created profiles of the user are private. **Note**: The private settings option can be activated only if the user has the right to maintain private settings (see User management).

The settings are grouped according to functionality. The following table gives an overview of the sections:

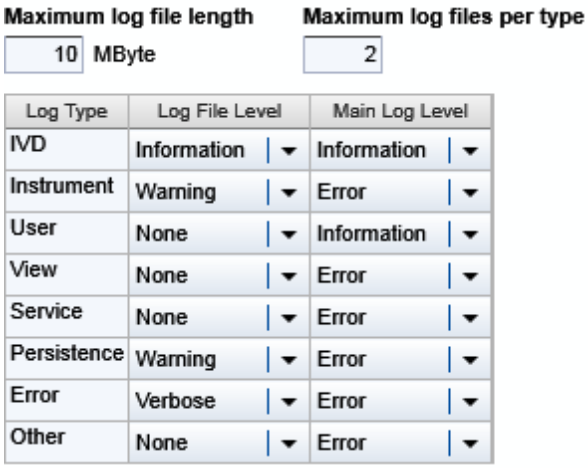
21 CFR Part 11 Support

Controls functionality required by 21 CFR Part 11 (FDA guidelines on electronic records). Select this option to enable auto-lock and to limit the number of failed logins.

Option	Description
AutoLock	The system automatically locks the QIAxcel ScreenGel software after the specified period of idle time, except when a process is running. To unlock, the user must login again. Refer to the User authentication section for more information about how to unlock. **Note:** Idle time means time without user action or instrument action.
Maximum number of failed logins	After the specified number of failed logins, the system automatically locks the user account. It can be unlocked by the administrator only.

Log files

The QIAxcel ScreenGel software writes all log messages to one main log file. In addition, separate log files can be created for individual log message types (IVD, Instrument, etc).



The size of a log file is limited; this size is configured by the "Maximum log file length". To always have the latest log files available, a new file will be created when the maximum size has been reached. The number of log files to be kept is configured by the "Maximum log files per type". When, for a particular log file type, the maximum number of files has been reached, the oldest file of that type will be deleted.

The verbosity increases from "Critical" to "Verbose". When "Critical" is selected, only critical log messages are written to the log file. When "Verbose" is selected, all log messages are written to the log file.

Note: The "Verbose" level can decrease the performance of the QIAxcel ScreenGel software.

The main log file gives an overview of the last actions in the software. The verbosity of the main log file is set in the "Main Log Level" column of the above table. This describes how much information of a log type will be added to the main log file. Keep the information as short as possible for each log type. Start with the levels as shown in the image above.

The verbosity of the individual log files is set in the "Log File Level" column. Increase the log level for special types of error tracking.

Log Type	Description
IVD	Audit trail. If this is also included in the main log file, it helps to understand the last actions.
Instrument	In case of communication problems, it can be useful to increase the "Log File Level" to "Verbose" for a certain time span, and to reproduce the situation. With these settings, the "Instrument" log file reaches the maximum log file length very soon (after one run). Therefore, disconnect from the instrument just after the situation occurred, export the log files, and return to verbosity "Warning". Use verbosity "Error" in the "Main Log Level" column to keep the overview character of the main log file.
User	Traces the user actions.
View	Information from the graphical user interface of the software.
Service	Information from the software logic.
Persistence	Information about loading and saving. Increase verbosity of the "Log File Level" if there are problems with loading and saving experiments or profiles.
Error	The "Log File Level" should be set to "Verbose" for detailed information in case of an error. The "Main Log Level" should be set to "Error" to keep the overview character of the main log file.
Other	All other information.

Refer to the Troubleshooting folder and log files section for information how to export log files.

Generate plate ID When enabled, defines how automatically generated plate IDs are constructed.

The following options define construction of the plate ID.

Option	Description
Cartridge ID	If this option is selected, the generated plate ID will contain the Cartridge ID at the start.
Date	If this option is selected, the generated plate ID will contain the date of the data acquisition. If Cartridge ID is included, the date will be placed next to the Cartridge ID.
Time or Counter	Specifies how the uniqueness of the plate ID is achieved: with the time of the process start (including hours, minutes, and seconds) or with the counter incremented for the next plate ID generation. **Note:** If the plate ID is edited during process setup after automatic generation, the time will not reflect the exact process start time, but will reflect the time the plate ID was generated during process setup.

The "Example" field shows what the generated plate ID may look like.

Sample Selection — Specifies which optional information can be entered at the "Sample Selection" screen of the process wizard.

Option	Description
Enable input fields for Buffer lot IDs	Select this option only, if you want to provide lot IDs for Buffers. If this option is not selected you cannot provide lot IDs for Buffers during process setup.
Enable input fields for Marker lot IDs	Select this option only, if you want to provide lot IDs for Markers. If this option is not selected you cannot provide lot IDs for Markers during process setup.
Provide Sample Information	Select this option, if you usually provide sample information. Even if this option is not selected you can provide sample information, but have to select the "Provide Sample Information" option at the "Sample Selection" screen of the process wizard manually.
Prevent modification of imported sample information	Select this option if you want sample information from imported rack files to be 'read only'.

Instrument

Option	Description
Latch cartridge automatically	If this option is selected, the system latches the cartridge automatically after a cartridge is inserted and the cartridge door is closed.
Perform calibration automatically	If this option is selected, the system performs cartridge calibration automatically, if the inserted cartridge has not yet been calibrated.

	COM Channel	Specifies the COM channel the QIAxcel Advanced instrument is connected to. After login, the system automatically tries to connect to the QIAxcel Advanced instrument using the specified COM port.
Rise Time	The rise time is a parameter of the Bessel filter applied to the raw data during acquisition. This parameter should not be changed unless you know the function of the Bessel filter and the effects of changes to the rise time parameter.	
Directories	Specifies the directories for acquired raw data and all other application data.	

The base directory for the directories listed below is initially (i.e., after the QIAxcel ScreenGel installation) the Application Data directory which is specified during the Installation of the ScreenGel software. All these directories are configurable.

The following directories can be specified:

Directory name	Description
Export	Default export directory. This is the default directory in which export files are generated, unless a different directory is chosen in the export profile.
Report	Default report directory. This is the default directory in which report files are generated, unless a different directory is chosen in the report profile.
Header & footer	Directory for report header and footer. During report generation the system looks here to find a header and footer to be included in the report.
Sample information	Default directory for importing or exporting sample information (see Running procedure or Running a process with advanced options, respectively). An example import "rack file" can be found in the default directory %DATA_DIR%\SampleInfo.
Troubleshooting	Directory where files created by the Troubleshooting folder are stored.
Experiment	Directory that contains 3 sub-directories: "DNA", "RNA", and "Protein". The experiment data files (both acquired as a process run result or combined in the "Analysis" environment) are saved by default in these sub-directories (according to the application mode), unless a different directory was chosen in the process profile.
Local Experiment	During a process, the experiment is saved in this directory. It is hard-coded to %DATA_DIR% \LocalExperiment. After the process has finished, the experiment is moved to the experiment path defined in the process profile. Only if this transfer fails (e.g., if it is a remote drive, and someone has tripped over the network cable), the experiment can still be found in the Local Experiment directory.

ExportTransformation Scripts	This directory contains XSLT scripts for transforming export XML files. XSLT is a declarative language that enables transformation of the export XML file into a different format, for example, another XML, HTML, or plain text. Some example XSLT files can be found in the default directory %DATA_DIR% \ReportExportProfile\XSLT_Export, for creating files in . csv format from the export.
ExportRawTransformationScripts	This directory contains XSLT scripts for transforming raw data export XML files. An example XSLT file can be found in the default directory %DATA_DIR% \ReportExportProfile\XSLT_RawExport, for creating a file in .csv format from the raw data export.

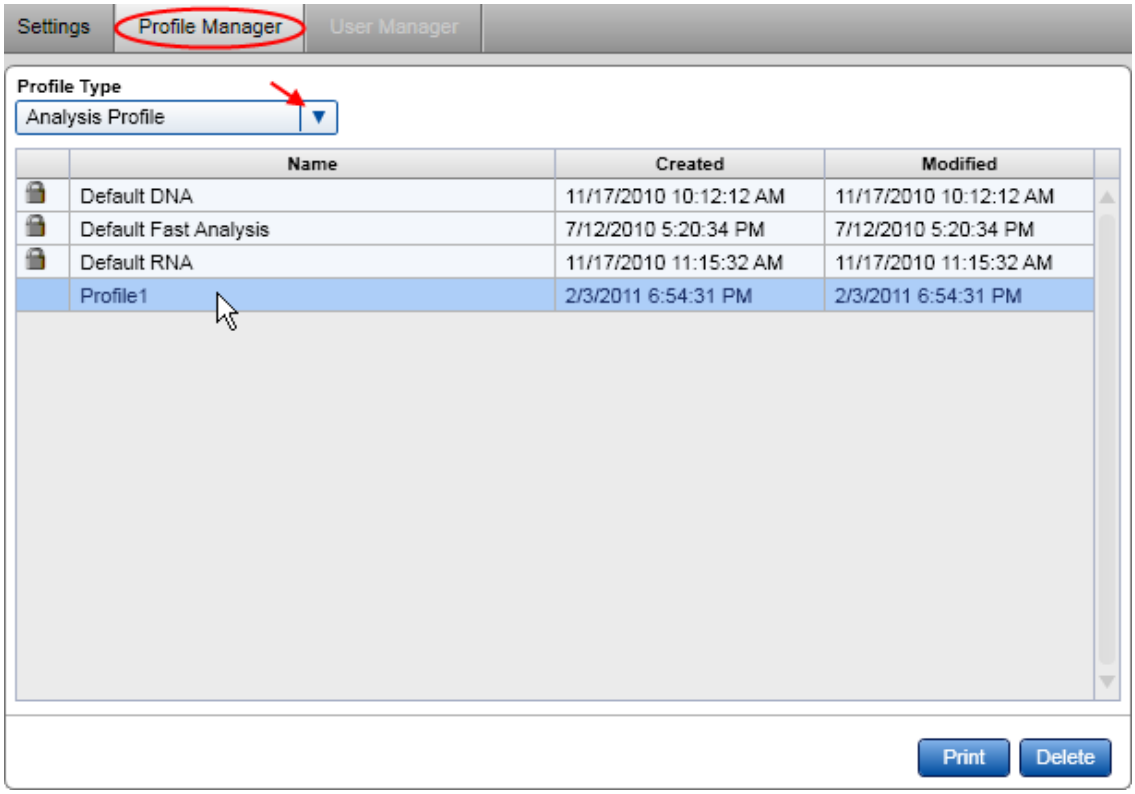
Note: The directories above can be opened in the Windows explorer directly from QIAxcel ScreenGel software through the menu item "File"/"Open Data Directory".

Most settings changes take immediate effect after clicking "OK". The following table lists settings that require additional actions:

Generate plate ID section	Active after next login.
Instrument - COM channel	Active after reconnection with instrument. **Note**: After clicking "OK", the system asks you to reconnect to the new COM channel.
Directories	Next login.

6.6.2 Profile management

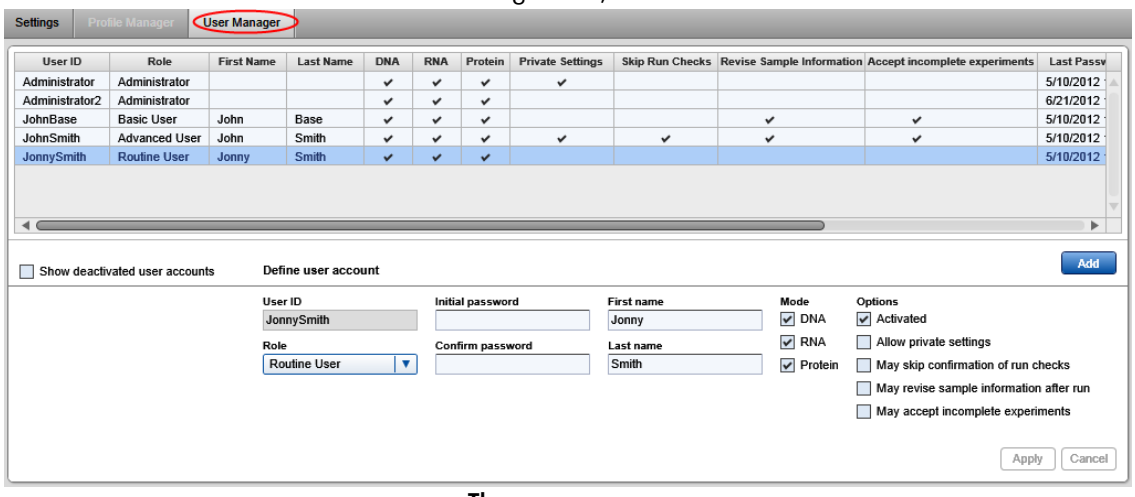
Several dialog boxes of the QIAxcel ScreenGel software allow the creation of new profiles, for example analysis profiles, size marker tables, and reference marker tables. The "Profile Manager" lists all profiles grouped by type. Profile details can be printed and profiles can be deleted using the "Profile Manager".



Note: Profiles that are marked with a padlock symbol are default profiles provided by QIAGEN. These profiles cannot be deleted.

6.6.3 User management

Administrators have access to the "User Manager" tab, in which user accounts can be modified:



The user manager.

Editing user accounts

To edit an existing user account:

1. Select the user account to be modified.
2. The details are displayed in the section at the bottom of the dialog box.
3. Modify the parameters as required.
4. Click the "Apply" button.

Note: In the "User manager", the user name, role, password, and authorizations of existing user accounts can be changed. The user ID (login name) is the unique identifier of a user and cannot be changed.

Adding users

To add a new user:

1. Click the "Add" button.
2. Specify a user ID not already in use, a user role, and a password. For details about user roles refer to the User roles section.

   Note: The password must contain one upper-case character, one lower-case character, and one digit. The minimum size of the password is eight characters.
3. Set the allowed run modes and user options.
4. Click the "Apply" button.

Note: You can create several user accounts for one person by giving the accounts different user IDs. This may be useful to distinguish different roles.

Deactivating user accounts

User accounts cannot be deleted, but they can be deactivated if users no longer work with QIAxcel ScreenGel Software data.

To deactivate a user account:

1. Select the user account to be deactivated from the list of users.
2. Uncheck the "Activated" option in the user settings. Deactivated users cannot log in anymore.
3. Click the "Apply" button.

Note: Only activated users are shown in the user table. To show deactivated users, check the "Show deactivated user accounts" checkbox below the user table.

User options

Allow private settings	Allows the user to maintain private settings.
May skip confirmation of run checks	On the "Run Check" page of the process wizard, the user may skip the confirmation of check messages.

May revise sample information after run	Enables the user to "Revise sample information" in the experiment explorer.
May accept incomplete experiments	If an experiment has run incompletely, the user can mark it as complete in the experiment explorer, overriding all warnings.

This page intentionally left blank

7. Maintenance Procedures

7 Maintenance Procedures

The following maintenance procedures must be carried out to ensure reliable operation of the QIAxcel Advanced:

- Cleaning of the QIAxcel Advanced
- Minor corrective maintenance

Following these procedures ensures that the QIAxcel Advanced is free of dust and liquid spills.

Important: Disconnect the line power cord from the power outlet before servicing.

Servicing

The QIAxcel Advanced is supplied with a warranty that lasts for 1 year, starting from the date of shipment. The warranty includes all repairs due to mechanical breakdown. Application development, software upgrades, accessories, and disposable items are not included in the warranty.

QIAGEN offers comprehensive Service Support Agreements, including Warranty Extensions, Full Cover Support Agreements, and instrument/application training, including on-site installation. Service Support Agreements maximize productivity and ensure high performance from your instrument. In addition, service histories are fully documented and all parts are certified and guaranteed.

Contact your local QIAGEN Field Service Specialist or your local distributor for more information about flexible Service Support Agreements from QIAGEN.

7.1 Cleaning of the QIAxcel Advanced

Cleaning agents

CAUTION	**Damage to the instrument** [C5] Do not use bleach, solvents, or reagents containing acids, alkalis, or abrasives to clean the QIAxcel Advanced.

WARNING	**Risk of electric shock** [W11] Do not open any panels on the QIAxcel Advanced other than described in this user manual. **Risk of personal injury and material damage** Only perform maintenance that is specifically described in this user manual.

Wipe the instrument with a damp cloth only.

The sample plate holder inside the instrument should be cleaned occasionally using a moist, soft cloth.

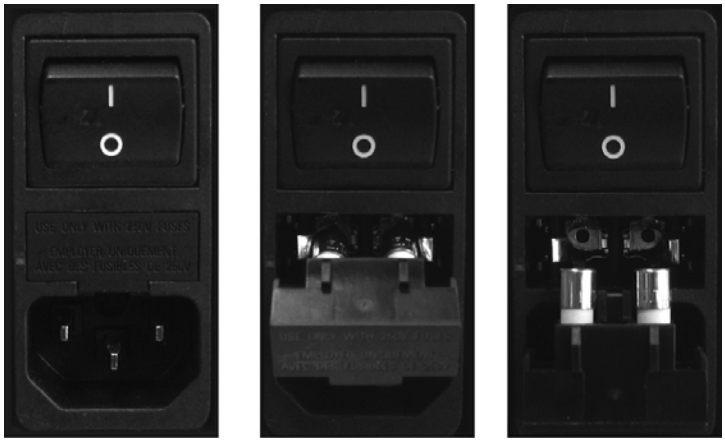
Wash the buffer tray in warm water using a mild detergent, rinse thoroughly with deionized water or reverse-osmosis water, and let it dry before filling with fresh buffer. The buffer tray should be cleaned before using a new QIAxcel gel cartridge.

7.2 Minor corrective maintenance

This section makes you familiar with the activities which may be required to maintain the QIAxcel Advanced or correct a failure.

7.2.1 Fuse replacement and cleaning

1. Switch off the QIAxcel Advanced using the main power switch.
2. Unplug the power cord from the power outlet and from the rear of the instrument.
3. Use a small flat-bladed screwdriver to remove the fuse-carrier assembly located above the area where the cord connector enters into the inlet.



Replacing the fuse.

4. Replace the fuse.
   Replace only with time-delay 4 Amp 250 V fuses, marked "T4A250V" cat no. 9241178. If replacement fuses are not available, contact QIAGEN Technical Services.
5. Reinsert the fuse-carrier assembly and plug in the power cord.
6. Turn on the power and check the instrument for normal operation, i.e. check that the status changes in the status panel (see section Operating the QIAxcel Advanced). If the instrument does not function normally, or continues to blow fuses, unplug the system and contact QIAGEN Technical Services.

7.2.2 N2 cylinder replacement

N_2 cylinders should be changed when one or both low pressure warnings are shown in the "Status Information" panel.

Remove the old N_2 cylinder:

Note: To remove a pressurized N_2 cylinder, empty the N_2 bottle first (see Empty N_2 bottle).

1. Open the sample door and remove the buffer tray.
2. Gently pull up on the N_2 cylinder port. Do not pull past the detent hole.
3. Turn the cylinder counter-clockwise to allow the remaining N_2 to gradually leak out.

   Note: Dispose of empty N_2 cylinders as recyclable steel material according to your local regulations.

Insert a new N_2 cylinder:

4. Screw a new, unpunctured N_2 cylinder into the cylinder port in a clockwise direction.

   Important: Only use N_2 cylinders provided by QIAGEN (cat no. 929705).

5. Turn until the needle inside the port punctures the N_2 cylinder. Do not over-tighten: the cylinder should only be finger tight.
6. Gently push down on the N_2 cylinder until it is in the stowed (down) position.

7.2.3 Alternate N2 supply

The QIAxcel Advanced external N_2 port (located at the rear of the instrument) can be supplied with clean, noncondensing compressed nitrogen. This external N_2 source can be used instead of the internal N_2 cylinder. The regulated N_2 minimum input pressure must be 50 psi (345 kPa) and the maximum input pressure should not exceed 75 psi (517 kPa).

To connect an external N_2 source, use the supplied urethane tubing (2 mm inner diameter x 3.18 outer diameter) rated for 150 psi. Additional tubing can be purchased separately (cat. no. 9018435).

Connect the urethane tubing from the output of the external N_2 source to the QIAxcel Advanced by firmly inserting the tubing into the fitting located on the rear panel of the instrument.

Turn on the external N_2 source pressure, and set the input pressure to 50–75 psi (345–517 kPa).

7.2.4 Blocked purge filter

Before a new sample run, fresh gel is purged from the gel reservoir of the cartridge into the capillaries by applying pressure through the purge line and purge port of the instrument. In rare cases when the QIAxcel gel cartridge was not stored in an upright position and equilibration conditions were not maintained, gel may run into the purge line of the instrument. A purge filter that is placed in the instrument prevents gel from running into the instrument's pressure valves. Gel in the filter or purge line will dry and thus block the filter or purge line.

To diagnose a blocked purge filter or purge line, the Filter Check with the QIAxcel ScreenGel Software can be performed. If the filter is blocked, a replacement of the purge filter is required. In very rare cases the purge line needs to be rinsed with water to resolve gel debris blocking the purge line tubing.

Note: Replacement of the purge filter and cleaning of the purge line is only required when the filter test failed and tubing is clogged.

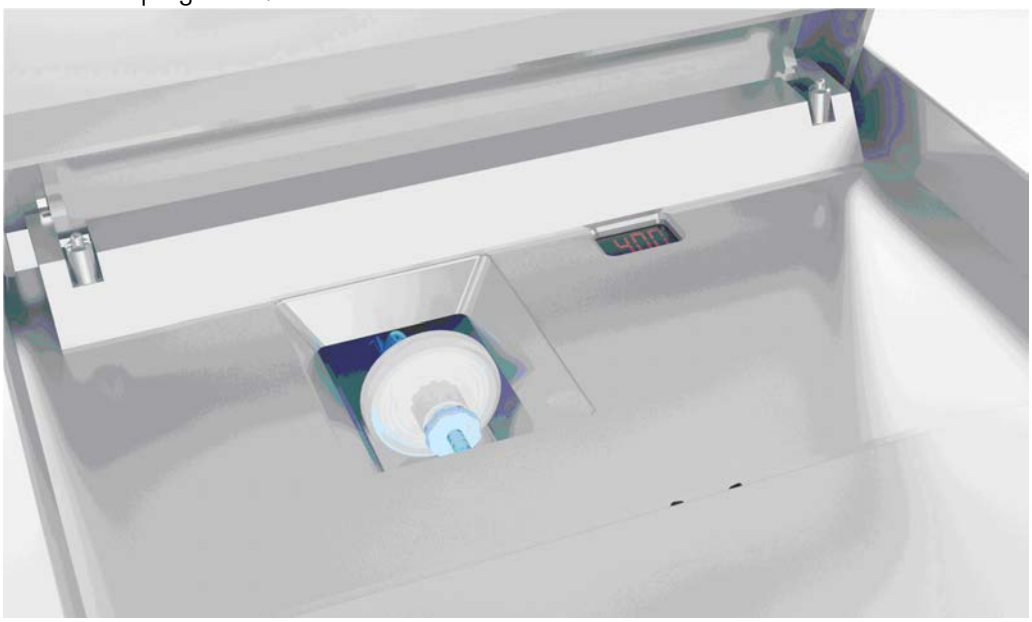
Note: It is not required to replace the purge filter or cleaning the purge line as a preventive maintenance.

Performing a Filter Check

1. Switch on the QIAxcel Advanced.
2. Launch the QIAxcel ScreenGel software .
3. Go to the System Check tab in the service environment and perform the guided Filter Check (see Filter check).
4. If Filter Check fails, replace the filter and test again.

Replacement of purge filter

1. Open the service door.
2. Remove the purge filter.



Note: Do not pull on the tubing.

3. Place a new purge filter and attach tightly to the connectors.
4. Perform the Filter Check again.

Note: If the Filter Check fails again, proceed with purge line cleaning procedure (see below).

Additional filters can be ordered from QIAGEN.

9021980 Set, Purge Filters (10), QX; please contact QIAGEN Technical Services.

Cleaning of the purge line

The Purge Line Cleaning Kit that is delivered with the QIAxcel Advanced instrument contains a cleaning insert, a 120 ml syringe, tubing and additional purge filters.

A vessel for collection (e.g., glass beaker) and deionised water must be provided by the user.

Proceed as follows:

1. Remove samples and the buffer tray from the instrument and close the sample door.
2. Remove the QIAxcel gel cartridge from instrument and place it in the QX Cartridge Stand (see Removing a QIAxcel gel cartridge).
3. Carefully wipe any gel debris from the receiver block and purge port.
4. Make sure you are logged in with user role "Advanced user" in "DNA" mode.
5. Place the cleaning insert into the cartridge bay and insert the attached smart key into the socket.

6. Close the cartridge door and click latch in the QIAxcel ScreenGel software.

   Note: Wait until latching is completed, approximately 10 seconds.

   Note: If auto latching is activated, the cleaning insert will automatically be latched after closing the cartridge door.
7. Open the cartridge door and check if the cleaning insert fits tightly and does not move.
8. Open the service door and remove the purge filter (see above).
9. Connect tubing to the connector close to the cartridge bay door and place the other end into an beaker (e.g).

   Note: Attaching the tubing to the wrong end facing rear of instrument can severely damage the instrument.
10. Fill the 120 ml syringe with deionised water and connect it to the tubing of the cleaning insert.
11. Pour water slowly and carefully through the tubing into the collection vessel.

    Note: There should be no observable resistance when water is poured through the tubing. If resistance is observed, only fill the tubing with a small volume of water and wait several minutes to allow dried gel to resolve. Try again to see if the resistance has gone. If not, contact QIAGEN Technical Services.
12. Wait for 10 minutes.
13. Fill syringe again and repeat rinsing procedure.
14. Fill the syringe with air and blow several times through the tubing until no more drops can be seen in the drain tubing.
15. Remove the drain tubing from the connector in the instrument.
16. Unlatch the cleaning insert and remove smart key and cleaning insert.

    Note: If auto latching is activated, the cleaning insert will be automatically unlatched after the smart key was removed.
17. Place a new purge filter (see above).

    Note: Attach the purge filter tightly and do not pull the tubing.
18. Close doors and perform the Filter Check again.

    Note: If the Filter Check fails again, contact QIAGEN Technical Services.

8. Troubleshooting

8 Troubleshooting

This section provides information about what to do if an error occurs when using the QIAxcel Advanced and QIAxcel ScreenGel.

If you need to contact QIAGEN Technical Services about an error, note down the steps leading to the error and the information from any dialog boxes that appear. This will help the QIAGEN Technical Service Specialist to resolve the error.

Refer to the Troubleshooting folder and log files section for detailed information on how to retrieve log files and system test results.

8.1 System setup

	Comments and suggestions
Instrument does not turn on	
a) Power cord not connected	Check the power connection.
b) Fuse blown	Replace the fuse.
Computer software cannot communicate with system	
a) RS232 cable is not connected between PC and system	Check the connection of the RS232 cable.
b) Incorrect COM port settings	Check the COM port setting (see section Settings).
c) Firmware version does not match the software version	If switching from QIAxcel ScreenGel software back to BioCalculator software version 3.2.05 or lower, switch the QIAxcel Advanced off and on at the power switch before launching BioCalculator software version 3.2.05 or lower.
d) Software cannot detect the COM port.	Check the user permission for the registry entries that are concerned the COM ports. The pertained registry entry is typically named *HKEY_LOCAL_MACHINE\SYSTEM\ControlSet001\Enum\ACPI\PNP0501\XXXXXX\Device Parameters*. Make sure that user "Everyone" has at least read permission for this entry, otherwise the COM port scan procedure (which is invoked at start of the application) might fail if the QIAxcel ScreenGel is being operated by a user who does not have administrator permissions.
No serial port in laptop computer	
Some laptops do not have a serial port	Contact the PC manufacturer to request the correct serial port connector.
QIAxcel ScreenGel software does not start	
a) QIAxcel ScreenGel software not installed	Install the QIAxcel ScreenGel software.
b) Old version of Microsoft Windows	The QIAxcel ScreenGel software operates with Windows XP and Windows 7 (see section Computer and software for more details).

8.2 Operation

	Comments and suggestions
N_2 cylinders do not last long	
a) Air leak	Double check the N_2 cylinder to make sure it is tight.
b) Internal leak if N_2 cylinder last only a couple of days	Contact QIAGEN Technical Services.
Samples tray does not move	
a) Transport lock is in place	Remove the transport lock.
b) Sample door is not closed	Close the sample door.
Cannot insert cartridge into system	
Cartridge installed backwards	Make sure the cartridge front cover faces the front of the system and check that the purge cap seal has been removed.
Cartridge cannot be latched	
a) N_2 pressure low	Replace the N_2 cylinder.
b) Cartridge door is open	Close the cartridge door.
c) Cartridge smart key not inserted	Insert the smart key.
Cannot run system	
a) Sample door and/or cartridge door are open	Close the sample door and/or cartridge door.
b) Cartridge smart key not detected	Insert the cartridge smart key
c) Pressure low	Replace the N_2 cylinder

8.3 DNA applications

	Comments and suggestions
DNA peaks signal variation in channels	
New cartridge requires calibration	Calibrate the cartridge (see section Calibrating a cartridge).
Slow peak migration time in channels	
a) Air bubbles in gel cartridge capillaries	Perform a purge or 3-minute purge (see Maintenance) to remove air bubbles, or change the QX Separation Buffer.
b) Current too low due to low temperature	Increase the room temperature.
c) Current too low due to partially dry capillary tips	Perform a purge or 3-minute purge to clean the capillary tips (see Maintenance).
Weak signal of the QX Alignment Marker	
Degraded/old QX Alignment Marker	Change the QX Alignment Marker.
No signal in channels	
a) No samples injected	Check the volume of sample (10 µl minimum).
b) Blocked capillary channel	Use the purge method to remove the blockage (see Maintenance). If this does not work, replace the cartridge.
c) Broken capillary or optical fiber in cartridge	Replace the cartridge.
d) Light source problem (LEDs off)	Check if all LEDs are illuminated. Contact QIAGEN Technical Services.
e) No purging of the cartridge/ purge filter blocked	Perform a Filter Check.
Loss of resolution in channels	
a) Old gel in some channels or clogged channels	Perform a purge or 3-minute purge to fill the channels with new gel, or repeat the purge method several times to remove clogging (see Maintenance).
b) Saturated signals	Reduce the sample injection time or select a more suitable method.
c) Expired cartridge	Use a new cartridge.
Broad or saturated DNA peak/band	
a) DNA concentration too high	Dilute the DNA solution in QX DNA Dilution Buffer. Reduce the injection time. Choose a method for high DNA concentration samples (e.g., 0H500 [see Appendix B]).

b) Broken channel with high background	Call QIAGEN Technical Services and replace cartridge.

DNA signal too low

a) DNA concentration too low	Increase the sample injection time. Choose a method for low DNA concentration samples (e.g., 0L500 [see Appendix B]).
b) Salt concentration too high in sample solution	Desalt or dilute the DNA samples to reduce the salt concentration and enhance DNA injection.

Separation current (µA) too low

a) QX Separation Buffer is contaminated	Replace the QX Separation Buffer.
b) Blocked capillary channel	Replace the QIAxcel gel cartridge.

Separation current (µA) too high

a) QX Separation Buffer contaminated	Replace the QX Separation Buffer.
b) Salt concentration too high in sample solution	Desalt or dilute the DNA samples in QX DNA Dilution Buffer.

Data squeezed together on gel image folder

a) Extra peaks before the first peak or after the last peak were detected	Remove the extra peaks and/or reset the parameter settings (see section Analysis).
b) Wrong peaks were identified as the first and last peaks for alignment	Remove the extra peaks and/or reset the parameter settings (see section Analysis).
c) Upper alignment markers were missing or below the threshold setting	Manually add the alignment marker and reprocess the data and replace the new markers for the next run.
d) Sample signals too strong and cause the alignment below the threshold setting	Dilute the samples or use the H Methods (see Appendix B) for sample analysis.

Data not aligned

a) Upper marker missing	Change to a new alignment marker.
b) Migration problem due to air bubbles	Purge and run the sample again.
c) Migration problem due to low temperature	Increase the separation time.
d) "Start Analysis" button in the "Analysis" environment not clicked	Click the "Start Analysis" button to perform analysis.

b) Broken channel with high background	Call QIAGEN Technical Services and replace cartridge.
e) Samples with different alignment markers visualized	Remove the samples with a different alignment marker from the view.
f) Alignment markers not identified correctly	Reanalyze the visualized samples with corrected peak detection parameters (alignment marker threshold, threshold; see Modifying an analysis profile). If necessary, correct the analysis result (add/delete peak; see Manually modifying analysis results).

No size calling in the result table

The reference marker is turned off	Select the right marker table.

Wrong size calling

a) Wrong reference marker table used	Select the right marker table.
b) Reference marker table setting problems	Make sure that the correct alignment marker is set (refer to Checking alignment marker). Make sure the number of peaks in the Rel. Time and size (bp) columns are equal in the reference marker table.

No size scale in gel image

a) Data not aligned	Remove from the view samples with a different alignment marker. Make sure all alignment marker peaks have been identified correctly.
b) Samples analyzed with different reference marker tables	Reanalyze the visualized samples with the same reference marker table.

Upper alignment markers resolved in double peaks

High salt sample	Dilute the sample or change the parameter setting.

8.4 RNA applications

	Comments and suggestions
Alignment is off	
a) The first peak is below the threshold	Decrease the threshold value (see section Modifying an analysis profile). Contamination, for example, by salt may result in aberrant migration of individual lanes that may be too large for proper alignment. Use less sample or perform an additional cleanup of RNA samples that show delayed migration.
b) Degraded/old calibration marker	Replace the calibration marker.
The ratio of rRNA (28S/18S) is too low	
Degraded RNA samples	Change the RNA sample.
The signal of RNA sample is too low	
a) Low RNA sample concentration	Increase the sample volume up to 5 µl. Mix an equal volume of RNA loading buffer to sample. For example, if 2 µl of RNA sample was used, mix the RNA sample with 2 µl of RNA loading buffer.
b) Degraded RNA samples	Change the RNA samples.
Broad RNA peaks	
a) Degraded RNA samples	Change the RNA samples.
b) Incomplete RNA denaturation process	Repeat the RNA denaturation process.
c) Aged buffer	Replace the separation buffer every 25 runs.
Only 18S RNA peak detected	
Incomplete RNA denaturation process	Repeat the RNA denaturation process. RNA degradation will also result in disappearance of the 28S peak first.
Calibration marker signal variation in channels	
a) New cartridge requires calibration	Calibrate the cartridge (see section Calibrating a cartridge).
b) Cartridge intensity calibration is incorrect	Calibrate the cartridge (see section Calibrating a cartridge).
c) Degraded/old QX Calibration Marker	Change the QX Calibration Marker.

	Comments and suggestions
Delayed peak migration in some channels	
a) Air bubbles in capillaries	Use the Long purge to remove air bubbles (see Maintenance).
b) Air bubbles in calibration marker or RNA sample vials	Remove the air bubbles from the vials.

8.5 Protein applications

	Comments and suggestions
Slow peak migration time in channels	
a) Air bubbles in gel cartridge capillaries	Perform a purge or long purge (see Maintenance) to remove air bubbles, or change the QX Separation Buffer.
b) Current too low due to partially dry capillary tips	Perform a purge or 3-minute purge to clean the capillary tips (see Maintenance).
Weak signal of the QX Pro Alignment Marker	
Degraded/old QX Pro Alignment Marker	Change the QX Pro Alignment Marker.
No signal in channels	
a) No samples injected	Check the volume of sample (10 µl minimum).
b) Blocked capillary channel	Use the purge method to remove the blockage (see Maintenance). If this does not work, replace the cartridge.
c) Broken capillary or optical fiber in cartridge	Replace the cartridge.
d) Light source problem (LEDs off)	Check if all LEDs are illuminated. Contact QIAGEN Technical Services.
e) No purging of the cartridge/ purge filter blocked	Perform a Filter Check.
Loss of resolution in channels	
a) Old gel in some channels or clogged channels	Perform a purge or 3-minute purge to fill the channels with new gel, or repeat the purge method several times to remove clogging (see Maintenance).
b) Expired cartridge	Use a new cartridge.
Broad or saturated protein peak/band	
a) Protein concentration too high	Dilute the protein in the sample with QX Pro Labeling Buffer. Reduce the injection time. Choose a method for high protein concentration samples (e.g., PH800s4kV [see Appendix B]).
b) Broken channel with high background	Call QIAGEN Technical Services and replace cartridge.
Protein signal too low	
a) Protein concentration too low after labeling	Increase the sample injection time. Choose a method for low protein concentration samples (e.g., PL800s4kV [see Appendix B]).
b) Salt concentration too high in sample solution	Desalt your protein sample by buffer exchange (gel filtration, ultrafiltration, precipitation).

	Comments and suggestions
c) Interfering substances in protein samples	Change buffer by gel filtration.
Separation current (µA) too low	
a) QX Pro Separation Buffer is depleted	Replace the QX Pro Separation Buffer.
b) Blocked capillary channel	Replace the QIAxcel gel cartridge.
Separation current (µA) too high	
a) QX Separation Buffer contaminated	Replace the QX Pro Separation Buffer.
b) Salt concentration too high in sample	Desalt the protein sample before the labeling reaction.
Artificial spike peaks occur	
a) Extra peaks not originating from the proteins in sample were detected	Remove the extra peaks and/or reset the parameter settings (see section Analysis).
Data squeezed together on gel image folder	
a) Extra peaks before the first peak or after the last peak were detected	Remove the extra peaks and/or reset the parameter settings (see section Analysis).
b) Wrong peaks were identified as the first and last peaks for alignment	Remove the extra peaks and/or reset the parameter settings (see section Analysis).
c) Upper or lower alignment markers were missing or below the alignment marker threshold setting	Manually add the alignment marker and reprocess the data.
Data not aligned	
a) Alignment marker peaks are missing	Replace alignment marker or edit alignment marker peaks manually (low peak height).
b) Migration problem due to air bubbles	Purge and run the sample again.
c) Migration problem due to low laboratory temperature	Increase the separation time.
d) Data analysis not carried out correctly	Repeat sample analysis (see section Analysis).
No size calling in the result table	
a) The reference marker is turned off	Select the right marker table and create a reference marker

	Comments and suggestions
b) Reference marker table setting problems	Make sure the number of peaks in the Rel. Time and size (bp) columns are equal in the reference marker table. Delete peaks, if necessary.
No size scale in gel image	
a) Data not aligned	Make sure all alignment markers have been identified correctly.
b) Samples analyzed with different reference marker tables	Reanalyze the visualized samples with the same reference marker table.
Proteins show shifted molecular weights	
a) Apparent molecular weight of protein differs from theoretical weight	Desalt your sample or dilute sample with QX Pro Labeling Buffer. Dilute the size marker to an appropriate concentration using the sample buffer of the respective protein (5 µl size marker + 15 µl sample buffer) before starting the labeling the reaction. Use the labeled size marker without any further dilution for analysis.

This page intentionally left blank

9. Glossary

9 Glossary

Term	Description
Buffer tray	The buffer tray is a removable plastic tray that sits in the buffer tray holder of the QIAxcel Advanced and holds QX Separation and Wash Buffers and QX Intensity and Alignment Markers.
Buffer tray holder	The buffer tray holder is located inside the QIAxcel Advanced under the sample door. The buffer tray, which holds QX Separation and Wash Buffers and QX Intensity and Alignment Markers, is placed in the buffer tray holder prior to sample analysis.
Cartridge door	The door that allows the QIAxcel gel cartridge to be loaded into the QIAxcel Advanced. This door should remain closed during operation of the QIAxcel Advanced.
Channel(s)	Each QIAxcel gel cartridge has 12 channels (capillaries) through which the samples for analysis pass.
Method	A method is the collection of commands and parameters that are applied to an individual sample run. A number of default methods are preinstalled.
Mineral oil	For covering solutions and/or samples to prevent evaporation.
N_2 door	The N_2 door, located to the right of the sample door, allows insertion and removal of the N_2 cylinder.
Position	An area of a rack/plate that can contain something. Examples of positions include the wells of a microplate or slots in the sample plate holder.
Power switch	A button located at the back of the QIAxcel Advanced in the bottom-left corner. It allows the user to switch the QIAxcel Advanced on and off.
"Process Profile"	This defines settings for data acquisition. Defines all parameters for the electrophoresis run.
Purge port	The purge port is located inside the QIAxcel Advanced instrument and aligns with the purge hole of the QIAxcel gel cartridge.
QX or QX Pro Alignment Marker	Allows sample migration time to be calibrated.
QX DNA or RNA Dilution Buffer	Allows dilution of concentrated samples.
QX DNA, RNA, or Pro Separation Buffer	Enables separation of DNA, RNA or protein molecules in the QIAxcel gel cartridge.
QX DNA or RNA Size Marker	Enables creation of a reference marker table allowing DNA/RNA size and/or concentration determination.
QX DNA, RNA or Pro Wash Buffer	For washing the capillary tips to prevent cross-contamination.

Term	Description
QX Intensity or QX Pro Calibration Marker	Allows calibration of the signal intensity for each new gel cartridge.
QX Pro Labeling Buffer	For protein denaturation and dilution
Sample door	The door that provides access to the sample plate holder and the buffer tray holder. This door should remain closed during operation of the QIAxcel Advanced.
Sample plate holder	The sample plate holder is located inside the QIAxcel Advanced under the sample door. 96-well plates or sample strips containing the samples for analysis are placed in the sample plate holder.
Service door	The service door allows access to the purge filter and a manometer.
Smart key	This key attached to the QIAxcel gel cartridge holds information about the cartridge (i.e., cartridge identifier, calibration status, number of runs). The smart key should be inserted into the smart key socket on the QIAxcel Advanced to enable sample analysis.
Smart key socket	The smart key socket allows the QIAxcel Advanced instrument to read and display the information on the smart key.

This page intentionally left blank

10. Appendices

10 Appendices

The appendices contain technical data, QIAxcel methods and accessories, descriptions of the data analysis algorithms, and warranty terms.

10.1 Appendix A

Technical data

QIAGEN reserves the right to change specifications at any time.

Environmental conditions

Operating conditions

Power	100–240 V AC, 50–60 Hz, 360 VA
Fuse rating	4 A (250 V) time-delay fuse (for 100–240 V AC)
Overvoltage category	II
Air temperature	15–30°C (59–86°F)
Relative humidity	10–75% (noncondensing)
Altitude	Up to 2000 m (6500 ft.)
Place of operation	For indoor use only
Pollution level	2
Environmental class	3K2 (IEC 60721-3-3)

Transportation conditions

Air temperature	–25°C to 60°C (–13°F to 140°F) in manufacturer's package
Relative humidity	Max. 75% (noncondensing)

Storage conditions

Air temperature	15°C to 30°C (59°F to 86°F) in manufacturer's package
Relative humidity	Max. 75% (noncondensing)

Mechanical data and hardware features

Dimensions (door closed)	Width: 370 mm (14.57 in.) Height: 405 mm (15.94 in.) Depth: 555 mm (21.85 in.)
Dimensions (doors open)	Width: 370 mm (14.57 in.) Height: 706 mm (27.80 in.) Depth: 555 mm (21.85 in.)
Mass	27 kg (59.52 lb.)
Capacity	Up to 96 samples per run
Software	Default protocols are provided with the QIAxcel ScreenGel software supplied with the QIAxcel Advanced. Updated protocols are available from www.qiagen.com/QIAxcelAdvanced.

Waste Electrical and Electronic Equipment (WEEE)

This section provides information about disposal of waste electrical and electronic equipment by users.

The crossed-out wheeled bin symbol (see below) indicates that this product must not be disposed of with other waste; it must be taken to an approved treatment facility or to a designated collection point for recycling, according to local laws and regulations.

The separate collection and recycling of waste electronic equipment at the time of disposal helps to conserve natural resources and ensures that the product is recycled in a manner that protects human health and the environment.

Recycling can be provided by QIAGEN upon request at additional cost. In the European Union, in accordance with the specific WEEE recycling requirements and where a replacement product is being supplied by QIAGEN, free recycling of its WEEE-marked electronic equipment is provided.

To recycle electronic equipment, contact your local QIAGEN sales office for the required return form. Once the form is submitted, you will be contacted by QIAGEN either to request follow-up information for scheduling collection of the electronic waste or to provide you with an individual quote.

FCC Declaration

The ''United States Federal Communications Commission'' (USFCC) (in 47 CRF 15. 105) declared that the users of this product must be informed of the following facts and circumstances.

This device complies with part 15 of the FCC. Operation is subject to the following two conditions: (1) This device may not cause harmful interference, and (2) this device must accept any interference received, including interference that may cause undesired operation.

This Class B digital apparatus complies with Canadian ICES-003.

The following statement applies to the products covered in this manual, unless otherwise specified herein. The statement for other products will appear in the accompanying documentation.

NOTE: This equipment has been tested and found to comply with the limits for a Class B digital device, pursuant to part 15 of the FCC Rules. These limits are designed to provide reasonable protection against harmful interference in a residential installation. This equipment generates, uses and can radiate radio frequency energy and, if not installed and used in accordance with the instructions, may cause harmful interference to radio communications. However, there is no guarantee that interference will not occur in a particular installation. If this equipment does cause harmful interference to radio or television reception, which can be determined by turning the equipment off and on, the user is encouraged to try to correct the interference by one or more of the following measures:

- Reorient or relocate the receiving antenna.
- Increase the separation between the equipment and receiver.
- Connect the equipment into an outlet on a circuit different from that to which the receiver is connected.
- Consult the dealer or an experienced radio/ TV technician for help.

QIAGEN GmbH, Germany is not responsible for any radio television interference caused by unauthorized modifications of this equipment or the substitution or attachment of connection cables and equipment other than those specified by QIAGEN GmbH, Germany. The correction of interference caused by such unauthorized modification, substitution or attachment will be the responsibility of the user.

Declaration of conformity

Name and address of the company

QIAGEN GmbH

QIAGEN Strasse 1

40724 Hilden

Germany

We herewith declare under our sole responsibility that the product

QIAxcel Advanced

meets all applicable requirements of the following European Directives

Low Voltage Directive (LVD)	**2006/95/EC**
Electromagnetic Compatibility Directive (EMC)	**2004/108/EC**

and the relevant harmonized standards

IEC 61010-1 (Ed. 2)

IEC 61010-2-081 (Ed.1)

IEC 61326-1

EN 61000-6-2

Hombrechtikon, April 1, 2011

CE

Pit Muggli

Senior Director Quality and Compliance Automated Systems

10.2 Appendix B

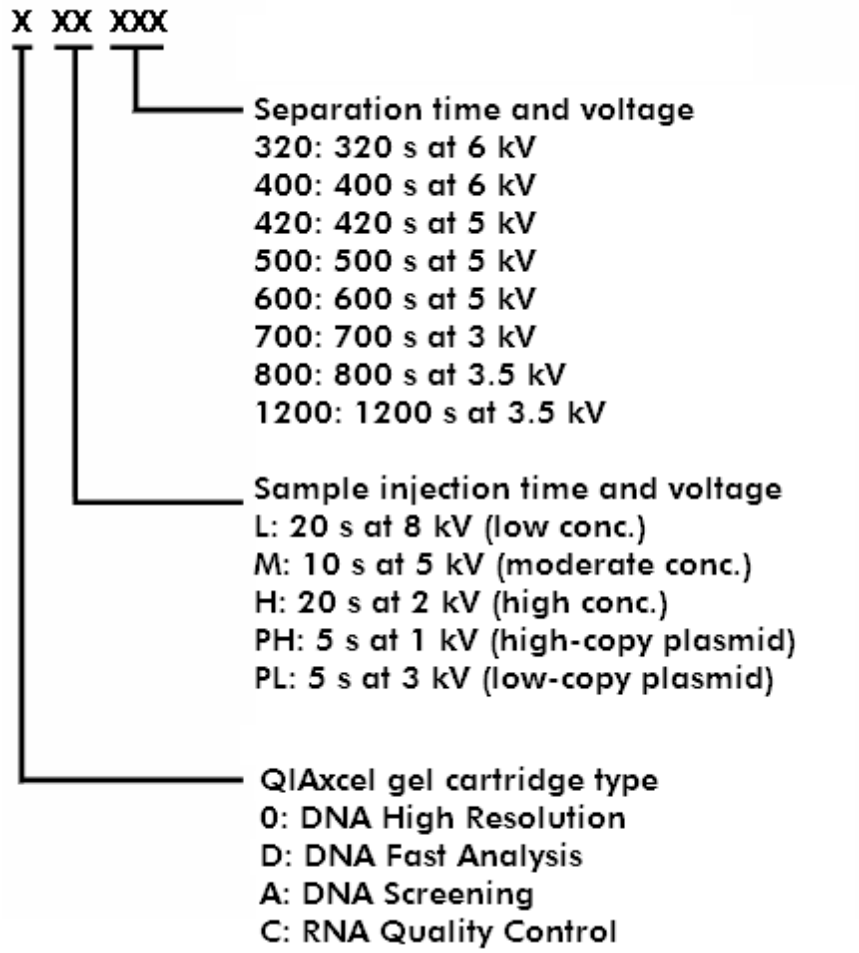
QIAxcel Advanced methods

A number of default methods are available for each QIAxcel Kit. Notice, that only the methods available for the particular cartridge type can be selected.

Note: If you require a custom method to be created, please contact QIAGEN Technical Services.

DNA/RNA methods

Each method name is an acronym, providing information on the specific QIAxcel Kit/QIAxcel gel cartridge being used, the sample injection time and voltage, and the separation time and voltage, as described below.


X XX XXX
Separation time and voltage
320: 320 s at 6 kV
400: 400 s at 6 kV
420: 420 s at 5 kV
500: 500 s at 5 kV
600: 600 s at 5 kV
700: 700 s at 3 kV
800: 800 s at 3.5 kV
1200: 1200 s at 3.5 kV
Sample injection time and voltage
L: 20 s at 8 kV (low conc.)
M: 10 s at 5 kV (moderate conc.)
H: 20 s at 2 kV (high conc.)
PH: 5 s at 1 kV (high-copy plasmid)
PL: 5 s at 3 kV (low-copy plasmid)
QIAxcel gel cartridge type
0: DNA High Resolution
D: DNA Fast Analysis
A: DNA Screening
C: RNA Quality Control

Description of method name acronyms.

Please find below a complete list of methods available for each QIAxcel gel cartridge type and information regarding their associated fragment sizes and best resolution.

QIAxcel DNA High Resolution methods

The QIAxcel DNA High Resolution Gel Cartridge is designed for high-resolution (3–5 bp) genotyping, high-resolution multiplex PCR, and AFLP/RFLP analysis of less than 20 fragments. The gel cartridge can separate fragment sizes ranging from 15 bp to 10 kb. The resolution depends on the fragment size and the method chosen to run the assay:

Guidelines for method selection using the QIAxcel DNA High Resolution Kit

	Fragment size			
	100–500 bp	**500 bp – 1 kb**	**1–5 kb**	**5–10 kb**
Method	**Best resolution**			
0M400* 0L400† 0H400‡	20 bp	100 bp	500 bp	N/A
0M500* 0L500† 0H500‡	10 bp	50 bp	200 bp	N/A
0M700* 0L700† 0H700‡	3–5 bp	N/A	N/A	N/A
0M800* 0L800† 0H800‡	3–5 bp	N/A	N/A	N/A
0M1200* 0L1200† 0H1200‡	N/A	N/A	500 bp – 1 kb	1– 1.5 kb

* We recommend the 0M400, 0M500, 0M700, 0M800, and 0M1200 methods for DNA concentrations of 10–100 ng/µl (e.g., PCR products amplified from genomic DNA with 30–40 cycles).

† We recommend the 0L400, 0L500, 0L700, 0L800, and 0L1200 methods for DNA concentrations of <10 ng/µl.

‡ We recommend the 0H400, 0H500, 0H700, 0H800, and 0L1200 methods for DNA concentrations of >100 ng/µl (e. g., high-yield PCR products).

M Methods

We recommend the 0M400, 0M500, 0M700, 0M800, and 0L1200 methods for DNA concentrations of 10–100 ng/µl.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)
0M400	5	10	6
0M500	5	10	5
0M700	5	10	3
0M800	5	10	3
0M1200	5	10	3.5

* Sample injection time can be adjusted (minimum 1 s; maximum 60 s). Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops. Increase sample injection time if the signal is below the default setting of the threshold of 5%.

L Methods

We recommend the 0L400, 0L500, 0L700, 0L800, and 0M1200 methods for DNA concentrations
of <10 ng/µl.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)
0L400	8	20	6
0L500	8	20	5
0L700	8	20	3
0L800	8	20	3
OL1200	8	20	3.5

* Sample injection time can be adjusted (minimum 1 s; maximum 60 s). Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops. Increase sample injection time if the signal is below the default setting of the threshold of 5%.

H Methods

We recommend the 0H400, 0H500, 0H700, 0H800, and 0H1200 methods for DNA concentrations of >100ng/µl.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)
0H400	2	20	6
0H500	2	20	5
0H700	2	20	3
0H800	2	20	3
0H1200	2	20	3.5

* Sample injection time can be adjusted (minimum 1 s; maximum 60 s). Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops. Increase sample injection time if the signal is below the default setting of the threshold of 5%.

Note: Unpurified PCR products contain dNTPs and primers, which can contribute to the optical density (OD) and cause over estimation of the DNA concentration.

QIAxcel DNA Screening methods

The QIAxcel DNA Screening Kit is designed for low-resolution (>20bp) genotyping, low-resolution multiplex PCR, single PCR screening, plasmid DNA digestion checking, and plasmid and oligo DNA quantity checking. The gel cartridge can separate the fragment size range from 15bp to 5kb. The resolution depends on the fragment size and the method chosen to run the assay:

Guidelines for method selection using the QIAxcel DNA Screening Kit

	Fragment size		
	<500 bp	500 bp – 1 kb	1–5 kb
Method	Best resolution		
AM320* AL320† AH320‡	20 bp	100 bp	500 bp
AM420* AL420† AH420‡	20 bp	100 bp	500 bp
APH600 APL600	Uncut plasmid DNA checking		

* The AM320 and AM420 methods are recommended for DNA concentrations 10–100 ng/µl (e.g., PCR products [30–40 cycles] amplified from genomic DNA).
† The AL320 and AL420 methods are recommended for DNA concentrations <10 ng/µl.
‡ The AH320 and AH420 methods are recommended for DNA concentrations >100 ng/µl (e.g., high-yield PCR products).

M Methods

The AM320 and AM420 methods are recommended for DNA concentrations 10–100 ng/µl, while method APH600 is recommended for purified high-copy plasmid DNA (50–300 ng/µl) in elution buffer.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)
AM320	5	10	6
AM420	5	10	5
APH600	1	5	6

L Methods

The AL320 and AL420 methods are recommended for DNA concentrations <10 ng/µl, while method APL600 is recommended for purified low-copy plasmid DNA (<50 ng/µl) in elution buffer.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)
AL320	8	20	6
AL420	8	20	5
APL600	3	5	6

* Sample injection time can be adjusted from 5 to 40 seconds to obtain optimal signals. Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops. Increase sample injection time if the signal is below the default setting of the threshold of 7%.

H Methods

The AL320 and AL420 methods are recommended for DNA concentrations >100ng/µl.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)
AH320	2	20	6
AH420	2	20	5

* Sample injection time can be adjusted from 5 to 40 seconds to obtain optimal signals. Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops. Increase sample injection time if the signal is below the default setting of the threshold of 7%.

Note: Unpurified PCR products contain dNTPs and primers, which can contribute to the optical density (OD) and cause overestimation of the DNA concentration.

QIAxcel DNA Fast Analysis methods

The QIAxcel DNA Fast Analysis Gel Cartridge is designed for rapid analysis of PCR fragments. The gel cartridge can separate fragments ranging from 15 bp to 3 kb in size.

Note: The QIAxcel DNA Fast Analysis Cartridge, QX DNA Size Marker 50 bp – 1.5 kb, and the corresponding methods are not suited for concentration determination.

Methods for use with the QIAxcel DNA Fast Analysis Cartridge

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)
DM80	15	8	15
DM80 v2.0†	15	8	15
DM150	10	10	10
DM190	10	15	10

* Sample injection time can be adjusted (minimum 1 s; maximum 40 s). To obtain optimal signals, we recommend using a minimum of 5 s and a maximum of 15 s.
† DM80 v2.0 includes a longer purge time between runs and thus improves the background level.

QIAxcel RNA Quality Control methods

The QIAxcel RNA Quality Control Gel Cartridge is designed for quality control of total RNA, cRNA, fragmented RNA, and single-stranded cDNA.

- Method CM-F-RNA is recommended for use with fragmented RNA and fragmented DNA at a concentration of 250–500 ng/µl.
- Method CM-RNA is recommended for use with total RNA at a concentration of 300–1000 ng/µl or cRNA at a concentration of 100–500 ng/µl.
- Method CL-RNA is recommended for use with total RNA at a concentration of 50–300 ng/µl or cRNA at a concentration of <100 ng/µl.

Note: Total RNA and cRNA concentrations >1 µg/µl should be diluted to 1 µg/µl in sterile DEPC water before denaturing.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)	Separation time (s)
CM-F-RNA	7	20	3	600
CM-RNA	5	20	6	600
CL-RNA	8	20	6	600

* Sample injection time can be adjusted from 5 to 40 seconds to obtain optimal signals. Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops. Increase sample injection time if the signal is below the default setting of the threshold of 7%.

Protein methods

Each protein method is an acronym providing information on the sample injection time and voltage, as well as the separation time and voltage as described below.

M Methods

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)	Separati time (s)
PM600s5kV	10	5	5	600
PM800s4kV	10	5	4	800
PM1000s3kV	10	5	3	1000
PM1200s4kV	10	5	4	1200

* Sample injection time can be adjusted (minimum 1 s; maximum 60 s). Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops, Increase sample injection time if the signal is below the default setting of the positive threshold.

L Methods

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)	Separation time (s)
PL600s5kV	10	10	5	600
PL800s4kV	10	10	4	800
PL1000s3kV	10	10	3	1000

* Sample injection time can be adjusted (minimum 1 s; maximum 60 s). Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops, Increase sample injection time if the signal is below the default setting of the positive threshold.

H Methods

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)	Separation time (s)
PH600s5kV	5	10	5	600
PH800s4kV	5	10	4	800
PH1000s3kV	5	10	3	1000

* Sample injection time can be adjusted (minimum 1 s; maximum 60 s). Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops, Increase sample injection time if the signal is below the default setting of the positive threshold.

10.3 Appendix C

QIAxcel accessories

Product	Contents	Cat. no.
QIAxcel Advanced	Automated system for fast and fully automated DNA fragment analysis or qualitative and quantitative RNA analysis, QIAxcel ScreenGel software, 1-year warranty on parts and labor	9001941
QIAxcel Advanced Priority Package	Capillary electrophoresis device: includes Priority Package with computer, QIAxcel ScreenGel Software, installation, training, 2-year warranty on parts and labor, and 2 preventive maintenance visits	9002124
QIAxcel Advanced Priority Package Plus	Capillary electrophoresis device: includes Priority Package Plus with computer, QIAxcel ScreenGel Software, installation, training, 3-year warranty on parts and labor, and 3 preventive maintenance visits	9002125
QIAxcel Kits		
QIAxcel DNA High Resolution Kit (1200)	QIAxcel DNA High Resolution Cartridge, Buffers, Mineral Oil, QX Intensity Calibration Marker, 12-Tube Strips	929002
QIAxcel DNA Screening Kit (2400)	QIAxcel DNA Screening Cartridge, Buffers, Mineral Oil, QX Intensity Calibration Marker, 12-Tube Strips	929004
QIAxcel DNA Fast Analysis Kit (3000)	QIAxcel DNA Fast Analysis Cartridge, Buffers, Mineral Oil, QX Intensity Calibration Marker, QX DNA Size Marker 50 bp – 1.5 kb, QX Alignment Marker 15 bp/3 kb, 12-Tube Strips	929008
QIAxcel RNA QC Kit v2.0 (1200)	For 100 runs of 12 samples: QIAxcel RNA Quality Control Cartridge, Buffers, Mineral Oil, QX Intensity Calibration Marker, QX RNA Alignment Marker, QX RNA Size Marker 200-6000 nt, QX RNA Denaturation Buffer, 12-Tube Strips	929104

QIAxcel Protein Kit (1200)	For 100 runs of 12 samples; comprises the QIAxcel Protein Cartridge Kit and the QIAxcel Protein Reagent Kit (includes buffers, markers, and labeling dye)	929204
DNA size markers		
QX DNA Size Marker pUC18/*Hae*III (50 µl)	DNA size marker with 9 fragments: 80–587 bp	929550
QX DNA Size Marker FX174/*Hae*III (50 µl)	DNA size marker with 11 fragments:72–1353 bp	929551
QX DNA Size Marker 25bp – 1.8 kb (50 µl)	DNA size marker with 12 fragments: 25bp – 1.8 kb	929552
QX DNA Size Marker 100 bp – 2.5 kb (50 µl)	50 µl DNA size marker with 14 fragments: 100 bp – 2.5 kb	929559
QX DNA Size Marker 25–500 bp v2.0	50 µl DNA size marker with 17 fragments: 25–500 bp	929560
QX DNA Size Marker 50–800 bp v2.0	50 µl DNA size marker with 11 fragments: 50–800 bp	929561
QX DNA Size Marker 250 bp – 4 kb v2.0	50 µl DNA size marker with 11 fragments: 250 bp – 4 kb	929562
QX DNA Size Marker 250 bp – 8 kb v2.0	50 µl DNA size marker with 11 fragments: 250 bp – 8 kb	929563
Alignment markers		
QX Alignment Marker 15 bp/600 bp (1.5 ml)	Alignment marker with 15 bp and 600 bp fragments	929530
QX Alignment Marker 15 bp/1 kb (1.5 ml)	Alignment marker with 15 bp and 1 kb fragments	929521
QX Alignment Marker 15 bp/3 kb (1.5 ml)	Alignment marker with 15 bp and 3 kb fragments	929522
QX Alignment Marker 15 bp/10 kb (1.5 ml)	Alignment marker with 15 bp and 10 kb fragments	929523
QX Alignment Marker 15 bp/5 kb (1.5 ml)	Alignment marker with 15 bp and 5 kb fragments	929524
QX Alignment Marker 50 bp/500 bp (1.5 ml)	Alignment marker with 50 bp and 500 bp fragments	929525
QX Alignment Marker 50 bp/1 kb (1.5 ml)	Alignment marker with 50 bp and 1 kb fragments	929526
QX Alignment Marker 15bp/400bp (1.5 ml)	Alignment marker with 15 bp and 400 bp fragments	929527

QX Alignment Marker 50 bp/3 kb (1.5 ml)	Alignment marker with 50 bp and 3 kb fragments	929528
QX Alignment Marker 50 bp/5 kb (1.5 ml)	Alignment marker with 50 bp and 5 kb fragments	929529
QX RNA Alignment Marker (1.5 ml)	1.5 ml RNA alignment marker	929510
QX Pro Alignment Marker (1.5 ml)	1.5 ml Protein Alignment marker	929531
Protein size marker		
QX Pro Marker 14–97 kDa	575 µg of QX Pro Marker 14–97 kDa for size and quantity determination (to be used in combination with the QIAxcel Protein Kit only)	929564
Calibration marker		
QX Intensity Calibration Marker (600 µl)	600 µl QX Intensity Calibration Marker	929500
QX Pro Calibration Marker (0.6 ml)	600 µl QX Pro Calibration Marker	929501
Buffers		
QX DNA Dilution Buffer (15 ml)	15 ml QX DNA Dilution Buffer	929601
QX RNA Dilution Buffer (15 ml)	15 ml QX RNA Dilution Buffer	929602
QX Separation Buffer (40 ml)	40 ml QX Separation Buffer	929603
QX Pro Separation Buffer (40 ml)	40 ml QX Pro Separation Buffer	929608
QX Pro Labeling Buffer (25 ml)	25 ml Pro Labeling Buffer	929609
QX Pro Labeling Dye	250 µg QX Pro Labeling Dye	929610
QX Pro Reduction Agent	75 mg QX Pro Reduction Agent	929611
QX FA Separation Buffer (40 ml)	40 ml QX Separation Buffer; for use with QIAxcel DNA Fast Analysis Cartridges	929610
QX Wash Buffer (40 ml)	40 ml QX Wash Buffer	929604
QX Mineral Oil (50 ml)	50 ml QX Mineral Oil	929605
Accessories		
QX Cartridge Stand	QX Cartridge Stand	929701
QX Cartridge Stand Cover	QX Cartridge Stand Cover	929707
QX Buffer Tray	QX Buffer Tray	929702
QX 0.2 ml 12-Tube Strip (80)	80 x QX 0.2 ml 12-Tube Strips	929703
QX Multicolor 0.2 ml 12-Tube Strip (80)	80 x QX Multicolor 0.2 ml 12-Tube Strips	929704

QX Nitrogen Cylinder (6)	6 x QX Nitrogen Cylinder	929705
QX Cartridge Purge Tool	QX Cartridge Purge Tool	9241169

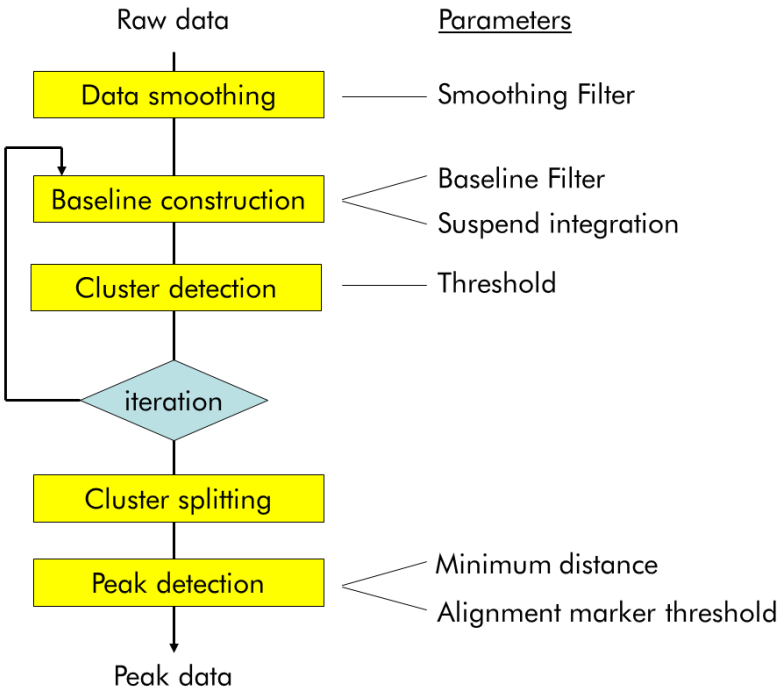
For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at www.qiagen.com or can be requested from QIAGEN Technical Services or your local distributor.

10.4 Appendix D

DNA analysis algorithm description

Summary

The figure below shows a flow diagram of the algorithm. The first step of the data analysis is smoothing. Then, an iterative approach is used to construct the baseline. The objective of this baseline construction is to effectively remove the peaks but accurately follow any other disturbances, e.g. baseline drift and shifts, in the electropherogram. The next step is the cluster detection. Clusters are defined as data subsets in the electropherogram where there is a certain minimal difference in signal between the actual data and the constructed baseline. In this step, no distinction is made between a single peak or multiple not baseline separated peaks. The next step is to split clusters that contain more than one peak. Finally, the actual peak detection is performed, in which peak apex, start point, end point and area are determined.



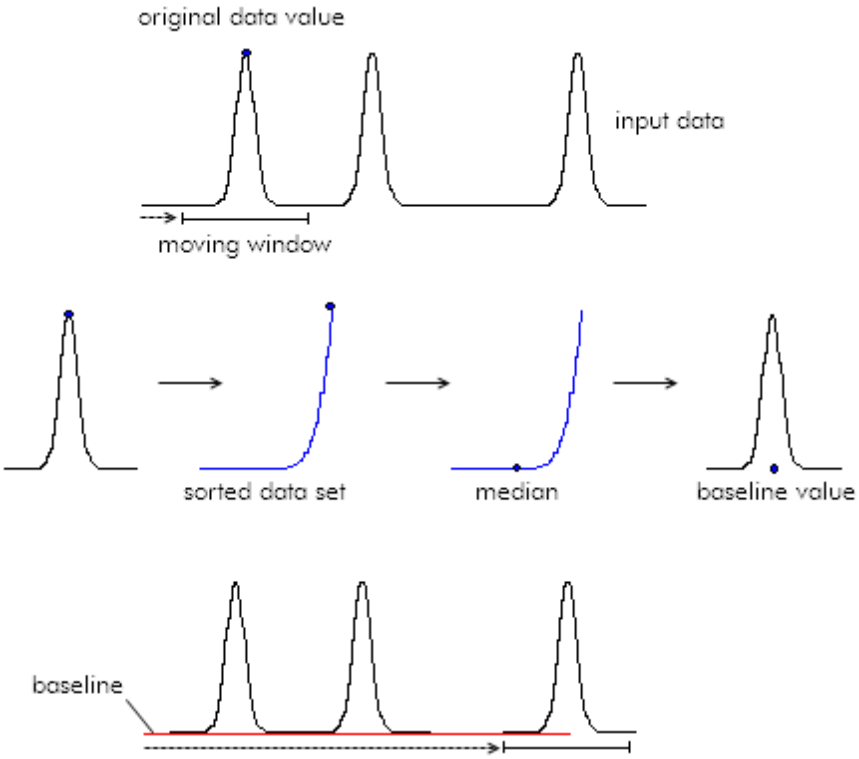
Smoothing

Smoothing is performed to increase the signal-to-noise ratio (S/N) of the data. The smoothing is performed with a Savitzky-Golay filter using a second order polynomial.

Baseline construction

The baseline construction is based on a moving median filter. The median of a dataset is defined as the center point of a dataset sorted in ascending order. A moving median filter processes the input data by replacing each data point by the median of a data subset centered around that datapoints.

If the original dataset is an electropherogram, the electrophoretic peaks will be sorted towards the high end because they have a higher intensity than the noise peaks. This means that as long as the size of the moving median filter (Filter Size) is at least twice the baseline peak width, datapoints of that peak will never reach the center (median) of the data subset, and will therefore be removed.



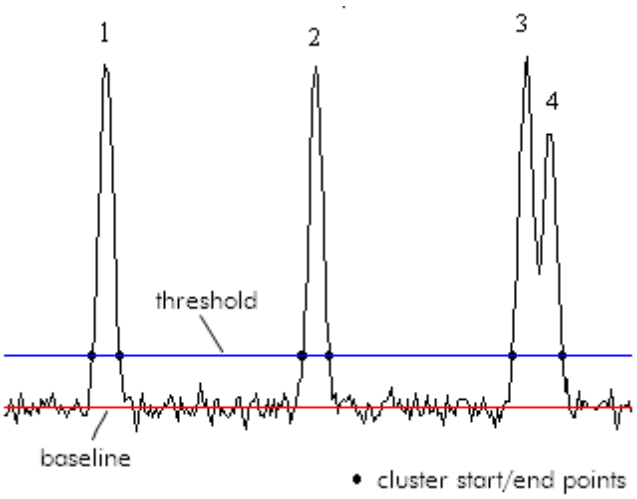
Mathematically the construction of the baseline using a moving median filter can be described as follows:

$$B(i) = \underset{x=i-r}{\overset{i+r}{Median}}(E(x))$$

in which B(i) represents the constructed baseline, E(i) the electropherogram, and r the filter rank.

Cluster detection

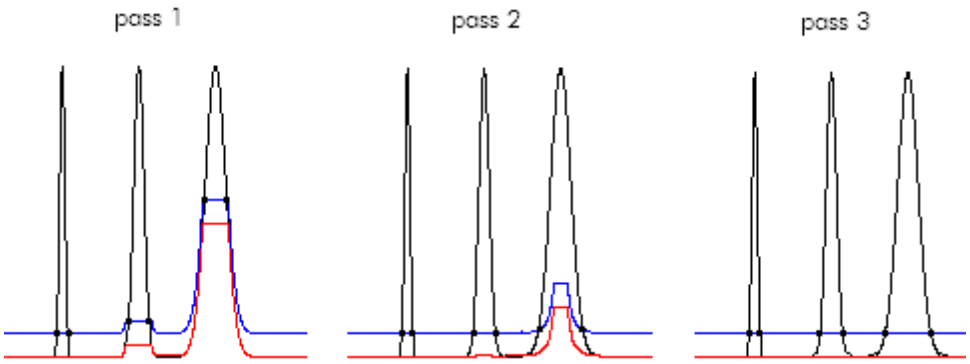
After the baseline construction, the actual peak detection is started. The first step of this process is called cluster detection. Clusters are defined as regions, i.e. data subsets, in the electropherogram where there is a significant difference between the raw data and the constructed baseline (see figure below). The parameter used to find these regions is the Threshold. The threshold is an imaginary line parallel to the constructed baseline, which marks the minimal height a peak must have (in reference to the constructed baseline) to be detected.



The identified regions can contain either one peak (peaks 1 and 2) or multiple, not baseline separated, peaks (peaks 3 and 4). In either case the region is called a cluster. Initially, the cluster start- and end points are marked as the points where the raw datapoints and the Minimum Peakheight threshold line cross.

The iteration process

As pointed out before, the successful removal of peaks during the baseline construction is dependent on the baseline filter size and peak width. In some cases it is not easy, or even impossible, to find a baseline filter size for optimal removal of all peaks in the electropherogram. This is especially the case in electropherograms with a wide variety of peak widths (requiring a large filter size on a very unstable baseline (requiring a small filter size to accurately preserve these relative high frequency baseline disturbances). The following Figure shows the effect of a too small filter size on the results of the baseline construction.



In the first pass, peak 1 is removed, but in peaks 2 and 3, the constructed baseline starts following the peak. Without any further modifications to the algorithm, this would result in inaccurate peak integration. To solve this problem the algorithm was made iterative. This means that multiple passes through the baseline construction and cluster detection are made, improving the baseline in each pass. The whole iteration process is based on the fact that even though the baseline construction during the first pass was not optimal, normally most of the clusters are still detected.

The principle of the iteration process is that the cluster information obtained in the previous pass is used to optimize the baseline construction in the current pass. In every additional pass, similar to the first pass, a moving median filter is used for the baseline construction. However, before determining the baseline, a check is made for overlaps between the clusters detected in the previous pass and the current filter position. If an overlap is detected, those points are deleted from the sorted data subset, leaving virtually only datapoints corresponding to baseline points in the original electropherogram. The value for the baseline is now determined by taking the median of this new shortened data subset.

The figure of pass 2 shows the new baseline calculated after two passes. The baseline under peak 2 is now correct but the baseline under peak 3 is still incorrect. Note, however, that the cluster start- and end points in peak 3 have shifted considerably closer to the correct position. A third pass therefore will remove a larger part of the peak from the sorted data subset leading to an improved baseline as shown after pass 3.

Cluster splitting

During the cluster detection, clusters with one or several peaks are determined. In cluster splitting step splits clusters with more than one peak into several clusters. This facilitates the peak detection in the next step. The algorithm used is very similar to the cluster detection algorithm. Cluster splitting is performed by iteratively increasing the threshold until clusters with more than one peak decompose to several clusters.

Peak detection

After the cluster splitting, each cluster contains exactly one peak. The apex of the peak is determined by looking up the maximum data point in the cluster. Then, the exact start- and end points of the peak are determined. Two criteria are used for this purpose; the first criterion locates the start- and end points of a cluster at the first point (in both directions, starting from the center of the cluster) were the raw data and the constructed baseline cross each other. The second criterion is used to detect cluster borders in case of overlapping peaks (where the raw data and baseline do not cross). In this case the start- and end points of a peak are located at the points where the absolute value of the first derivative remains below a certain threshold for several datapoints. Starting at the center of the cluster, the actual start- and end points of a cluster are found at the first points where one of these two criteria is met.

Note: During the peak detection, peaks that are too close to each other are merged (based on the *Minimum distance* parameter). To ensure detection of overlapping peaks, make sure that the value of the *Minimum distance* is less than the distance between two peaks. Lower the *Minimum distance* if necessary, especially if your peaks are very sharp and closely resolved.

10.5 Appendix E

Liability clause

QIAGEN shall be released from all obligations under its warranty in the event repairs or modifications are made by persons other than its own personnel, except in cases where the Company has given its written consent to perform such repairs or modifications.

All materials replaced under this warranty will be warranted only for the duration of the original warranty period, and in no case beyond the original expiration date of original warranty unless authorized in writing by an officer of the Company. Read-out devices, interfacing devices and associated software will be warranted only for the period offered by the original manufacturer of these products. Representations and warranties made by any person, including representatives of QIAGEN, which are inconsistent or in conflict with the conditions in this warranty shall not be binding upon the Company unless produced in writing and approved by an officer of QIAGEN.

10.6 Appendix F

Informations de sécurité

Avant d'utiliser le QIAxcel Advanced, il est impératif de lire attentivement ce manuel et de porter une attention particulière aux informations de sécurité. Afin de garantir un fonctionnement de l'appareil en toute sécurité et de maintenir l'appareil en bon état de marche, il est impératif de suivre les instructions et les informations de sécurité fournies dans le présent manuel d'utilisation.

Les types d'informations de sécurité suivants sont fournis tout au long du manuel.

WARNING	La formule « WARNING » (DANGER) est utilisée pour avertir des situations pouvant occasionner des dommages corporels à l'utilisateur ou à d'autres personnes. Les détails sur ces circonstances sont donnés dans un encadré semblable à celui-ci.

CAUTION	Le terme « CAUTION » (AVERTISSEMENT) est utilisé pour signaler les situations susceptibles de provoquer des détériorations de l'instrument ou d'autre matériel. Les détails sur ces circonstances figurent dans un encadré semblable à celui-ci.

Les conseils donnés dans ce manuel ont pour but de venir compléter les exigences de sécurité habituelles en vigueur dans le pays de l'utilisateur et non de s'y substituer.

Utilisation appropriée

WARNING/ CAUTION	**Risque de dommages corporels et matériels** **[W1]** L'utilisation non convenable du QIAxcel Advanced peut causer des blessures ou des détériorations de l'instrument. Le QIAxcel Advanced ne doit être utilisé que par du personnel qualifié qui a été formé de façon appropriée. Seul un ingénieur du service après-vente QIAGEN est autorisé à effectuer des travaux d'entretien sur le QIAxcel Advanced.

Procéder à la maintenance comme décrit dans la section « Maintenance Procedures » (Procédures de Maintenance). QIAGEN facture les réparations rendues nécessaires suite à une maintenance inappropriée.

WARNING/ CAUTION	**Risque de dommages corporels et matériels** **[W2]** Le QIAxcel Advanced est trop lourd pour être soulevé par une personne. Pour éviter des dommages corporels ou matériels, ne pas soulever l'instrument tout seul.

WARNING/ CAUTION	**Risque de dommages corporels et matériels** **[W3]** Ne pas essayer de bouger le QIAxcel Advanced pendant son fonctionnement.

CAUTION	**Détérioration de l'appareil** [C1] Eviter de renverser de l'eau ou des substances chimiques sur le QIAxcel Advanced. Tout dommage causé par de l'eau ou des produits chimiques mettra fin à la garantie.

En cas d'urgence, éteignez le QIAxcel Advanced à l'aide de l'interrupteur d'alimentation situé à l'arrière de l'appareil et débranchez le câble d'alimentation de la prise de courant.

CAUTION	**Détérioration de l'appareil** [C2] Si « Pressure 1» indique « Low » (bas) augmentez la pression du système avant d'utiliser la commande « unlatch » (décrochage). En enlevant la cartouche et la décrochant à pression réduite, l'appareil peut se déteriorer.

Sécurité électrique

Avant l'entretien, débranchez le cordon d'alimentation de la prise de courant.

WARNING	**Risque d'électrocution** [W4] Toute interruption du conducteur de protection à l'intérieur ou à l'extérieur de l'instrument, ou déconnexion du raccord du conducteur de protection (terre) peut rendre l'instrument dangereux. Il est interdit d'interrompre volontairement ce conducteur. **Présence de tensions mortelles dans l'instrument** Lorsque l'instrument est relié au secteur, les raccords peuvent être sous tension, et des parties sous tension peuvent être découvertes en ouvrant des capots ou en retirant des pièces (à l'exception de celles auxquelles il est possible d'accéder manuellement).

Afin que le QIAxcel Advanced fonctionne de manière satisfaisante et en toute sécurité, conformez-vous aux conseils suivants :

- Le câble d'alimentation doit être relié à une prise d'alimentation disposant d'un conducteur de protection (terre/masse).
- Ne réglez ni ne remplacez aucune pièce interne à l'appareil.
- Ne faites pas fonctionner l'appareil si des capots ou des pièces ont été retirés.
- Si du liquide a été renversé à l'intérieur de l'appareil, éteignez-le et débranchez-le de la prise d'alimentation, puis contactez le support technique de QIAGEN.
- Si vous remplacez les fusibles, ne les remplacer qu'avec des fusibles du même type et équivalent en voltage, comme indiqué sur le fusible.

Si l'appareil devient dangereux sur le plan électrique, empêchez d'autres membres du personnel de l'utiliser et contacter le support technique de QIAGEN ; l'appareil peut être dangereux électriquement si :

- celui-ci ou le câble d'alimentation semble endommagé ;
- il a été stocké dans des conditions défavorables pendant une longue période ;
- il a subi des chocs sévères durant le transport.

Environnement

Conditions de fonctionnement

WARNING	**Atmosphère explosive** [W5] Le QIAxcel Advanced n'est pas conçu pour fonctionner dans une atmosphère explosive.

WARNING	**Risque d'explosion** [W6] Le QIAxcel Advanced a été conçu pour l'utilisation des réactifs et substances fournis par les kits QIAxcel. L'utilisation des réactifs et substances autres que celles indiquées peut entrainer un risque d'incendie ou d'explosion.

CAUTION	**Détérioration de l'appareil** [C3] La lumière directe du soleil peut décolorer des parties de l'instrument et endommager des parties en plastique. Placer le QIAxcel Advanced en dehors de la lumière directe du soleil.

CAUTION	**Déterioration de la cartouche** [C4] Lors de l'utilisation de la cartouche de Gel, ne pas la laisser plus de 15 minutes hors de la position d'arrêt (« Wash park ») du compartiment des liquides. Au-delà de cette période, les extrémités des capillaires risquent de se dessécher et d'influencer le bon fonctionnement de la cartouche. Des capillaires desséchés mettront fin à la garantie. Les extrémités des capillaires sont en verre et sont très fragiles. Faites attention à ne pas heurter une surface dure. Cela pourrait les casser et influencer le bon fonctionnement de la cartouche. Des extrémités de capillaires cassées mettront fin à la garantie.

CAUTION	**Déterioration de la cartouche** [C4] Si vous utilisez moins de 12 échantillons, les puits vides doivent être remplis de tampon de dilution QX ADN ou ARN. Si les puits restent vides, les capillaires non-utilisés peuvent s'abîmer.

Produits chimiques

WARNING	**Substances chimiques dangereuses** **[W7]** Certaines substances chimiques utilisées avec cet instrument peuvent être dangereuses ou peuvent le devenir après que le protocole ait été effectué. Toujours porter des lunettes de protection, deux paires de gants et une blouse de laboratoire. La personne responsable (par exemple le Chef du laboratoire) doit prendre les précautions nécessaires pour assurer la sécurité de l'environnement du poste de travail et pour être sûr que les opérateurs de l'instrument sont suffisamment formés et non exposés à des quantités dangereuses de substances toxiques (chimiques ou biologiques) comme défini dans « Material Safety Data Sheets (MSDS) » ou des documents « OSHA, ACGIH ou COSHH ». L'évacuation des vapeurs et déchets doit être conforme à tous règlements et dispositions légales - au plan national, départemental et local - concernant la santé et la sécurité.

* OSHA: Occupational Safety and Health Administration (United States of America).
† ACGIH: American Conference of Government Industrial Hygienists (United States of America).
‡ COSHH: Control of Substances Hazardous to Health (United Kingdom).

WARNING	**Risque de feu** **[W8]** Lors du nettoyage du QIAxcel Advanced avec un désinfectant à base d'alcool, laisser la porte du QIAxcel Advanced ouverte pour permettre aux vapeurs inflammables de s'évaporer.

Mise au rebut des déchets

Les consommables et flacons utilisés peuvent contenir des agents chimiques dangereux. Ces déchets doivent être convenablement collectés et mis au rebut conformément aux règles de sécurité locales.

Pour savoir comment mettre au rebut le QIAxcel Advanced, voir l'annexe A (« Appendix A »).

Dangers mécaniques

La porte à cartouche et la porte à échantillons du QIAxcel Advanced doivent être fermées à tout moment pendant l'usage de l'instrument.

WARNING	**Eléments mobiles** **[W9]** Afin d'éviter tout contact avec les éléments mobiles du QIAxcel Advanced lorsqu'il est en marche, toujours fermer les portes de l'instrument pour les échantillons et pour la cartouche. Si les détecteurs ne fonctionnent pas correctement, contacter le Support Technique QIAGEN.

Symboles sur le QIAxcel Advanced

Symbole	Emplacement	Description
	Plaquette à l'arrière de l'appareil	Marquage CE
	Plaquette à l'arrière de l'appareil	Marquage CSA pour le Canada et les Etats-Unis
	Plaquette à l'arrière de l'appareil	Fabricant légal
	Plaquette à l'arrière de l'appareil	Symbole DEEE
	Plaquette à l'arrière de l'appareil	Marquage FCC de la commission fédérale des communications des Etats Unis

10.7 Appendix G

Sicherheitshinweise

Vor der Inbetriebnahme des QIAxcel Advanced sollten Sie dieses Handbuch sorgfältig durchlesen – beachten Sie insbesondere die Sicherheitshinweise. Die Gebrauchsanweisungen und Sicherheitshinweise im Handbuch müssen befolgt werden, um einen sicheren Betrieb des Geräts zu gewährleisten und das Gerät in einem sicheren Zustand zu erhalten.

In diesem Handbuch werden die folgenden beiden Kategorien von Sicherheitshinweisen verwendet:

WARNING	„WARNING“ (WARNUNG) weist auf Situationen und Umstände hin, die zu einer Verletzung des Benutzers oder anderer Personen führen können. Nähere Angaben zu der Art der Gefährdung und der Vermeidung solcher Situationen werden in einem Textfeld wie diesem neben der Warnung gemacht.

CAUTION	Der Begriff „CAUTION“ (ACHTUNG) weist Sie auf Situationen hin, in denen das Gerät oder andere Geräte beschädigt werden könnten. Nähere Einzelheiten über diese Situationen werden in einem Textfeld wie diesem beschrieben.

Die in diesem Handbuch enthaltenen Hinweise stellen eine Ergänzung und keinen Ersatz der üblichen Sicherheitsanforderungen dar, die im jeweiligen Land gelten.

Sachgemäße Handhabung

WARNING/ CAUTION	**Verletzungsgefahr und Beschädigung des Gerätes** **[W1]** Die unsachgemäße Bedienung des QIAxcel Advanced kann zu einer Verletzung des Benutzers oder zur Beschädigung des Gerätes führen. Die Bedienung des QIAxcel Advanced darf nur durch qualifiziertes Personal, das entsprechend geschult wurde, erfolgen. Die Wartung des QIAxcel Advanced darf nur durch Mitarbeiter des QIAGEN Kundendienstes durchgeführt werden.

Führen Sie alle Wartungsarbeiten gemäß den Anweisungen in Abschnitt „Maintenance Procedures “ (Wartungsarbeiten) dieses Handbuchs durch. QIAGEN stellt alle Reparaturen in Rechnung, die nachweislich auf eine inkorrekte Wartung zurückzuführen sind.

WARNING/ CAUTION	**Verletzungsgefahr und Beschädigung des Gerätes** **[W2]** Der QIAxcel Advanced ist zu schwer um von einer Person gehoben zu werden. Um Verletzungen des Benutzers oder eine Beschädigung des Gerätes zu vermeiden ist davon abzusehen, das Gerät alleine zu heben.

WARNING/ CAUTION	**Verletzungsgefahr und Beschädigung des Gerätes** [W3] Den QIAxcel Advanced während eines Laufes nicht bewegen.

CAUTION	**Beschädigung des Gerätes** [C1] Vermeiden Sie es, Wasser oder Chemikalien auf dem QIAxcel Advanced zu verschütten. Durch verschüttetes Wasser oder verschüttete Chemikalien verursachte Geräteschäden sind nicht durch die Garantie abgedeckt.

Schalten Sie im Notfall den QIAxcel Advanced aus (der Netzschalter befindet sich auf der Geräterückseite), und ziehen Sie den Netzstecker aus der Steckdose.

CAUTION	**Beschädigung des Gerätes** [C2] Wenn die Statusanzeige „Pressure 1" „Low" (niedrig) anzeigt, erhöhen Sie den Systemdruck bevor Sie „unlatch" (Entriegelung) auslösen. Das Herausnehmen der Kartusche und die Entriegelung bei niedrigem Druck kann das Gerät beschädigen.

Schutz vor Stromschlag

Ziehen Sie die Netzanschlusskabel aus den Steckdosen, bevor Sie Wartungsarbeiten am Gerät vornehmen.

WARNING	**Gefährdung durch Elektrizität** [W4] Jede Unterbrechung des Schutzleiters (Erdungs- bzw. Masseleiter) im Gerät oder außerhalb des Geräts und jede Abtrennung des Schutzleiters am Anschluss der Netzleitung erhöht die Gefahr eines Stromschlags. Eine absichtliche Unterbrechung der Schutzleiterverbindung ist verboten. **Gefährliche Spannung im Gerät** Auch in ausgeschaltetem Zustand kann an einigen Stellen im Gerät Netzspannung anliegen, wenn das Gerät am Stromnetz angeschlossen ist. Das Öffnen oder Entfernen von Gehäuseteilen kann diese stromführenden Teile freilegen.

Um einen zufriedenstellenden und sicheren Betrieb des QIAxcel Advanced zu gewährleisten, befolgen Sie bitte die nachstehenden Hinweise:

- Die Geräte-Netzkabel müssen an Wechselstrom-Steckdosen mit Schutzleiter (Erdungs-/ Masseleiter) angeschlossen werden.
- Nehmen Sie im Geräteinneren keine Einstellungen an Teilen vor und wechseln Sie keine Teile aus.
- Nehmen Sie das Gerät nicht in Betrieb, wenn Abdeckungen oder Teile entfernt worden sind.
- Falls Flüssigkeit auf dem Gerät verschüttet wird und in das Gerät läuft, dann schalten Sie es sofort aus, trennen Sie es von der Netzspannung (Stecker ziehen!) und setzen Sie sich mit dem Technischen Service von QIAGEN in Verbindung.
- Beim Austausch der Netzsicherung ersetzen Sie diese nur durch eine desselben Typs und der Stromstärke, die auf dem Etikett/Typenschild angegeben ist.

Falls die elektrische Sicherheit bei der Bedienung des Geräts nicht mehr gewährleistet werden kann, muss das Gerät gegen unbefugte oder unabsichtliche Benutzung gesichert werden. Kontaktieren Sie anschließend den Technischen Service von QIAGEN. Die elektrische Sicherheit des Geräts ist nicht mehr gegeben, wenn:

- das Gerät oder das Netzkabel beschädigt erscheint;
- das Gerät längere Zeit unter ungünstigen Bedingungen gelagert wurde;
- das Gerät unsachgemäß transportiert worden ist.

Umgebungsbedingungen

Betriebsbedingungen

WARNING	**Explosionsfähige Atmosphären** **[W5]** Der QIAxcel Advanced darf nicht in explosionsfähigen Atmosphären betrieben werden.

WARNING	**Explosionsgefahr** **[W6]** Der QIAxcel Advanced ist ausschließlich mit Reagenzien und Substanzen aus den QIAxcel Kits zu benutzen. Die Benutzung von anderen Reagenzien oder Substanzen kann Feuer oder eine Explosion auslösen.

CAUTION	**Beschädigung des Gerätes** **[C3]** Direktes Sonnenlicht kann Teile des Gerätes bleichen und Plastikteile schädigen. Der QIAxcel Advanced darf nicht ins direkte Sonnenlicht gestellt werden.

CAUTION	**Beschädigung der Kartusche** **[C4]** Die Gel Cartridge sollte nicht länger als 15 Minuten außerhalb der Parkposition („Wash park") des Solution Trays aufbewahrt werden. Wird dieser Zeitrahmen überschritten, trocknen die Spitzen der Kapillaren aus. Ausgetrocknete Kapillarspitzen sind nicht durch die Garantie abgedeckt. Die Kapillarspitzen sind aus Glas und sehr zerbrechlich. Achten Sie darauf, die Spitzen nicht auf harte Oberflächen aufzusetzen. Dadurch können die Kapillaren brechen und damit die Funktion der Cartridge beeinträchtigen. Zerbrochene Kapillarspitzen sind nicht durch die Garantie abgedeckt.

Chemikalien

WARNING	**Gefährliche Chemikalien** [W7] Einige der in Verbindung mit diesem Gerät verwendeten Chemikalien sind gesundheitsgefährdend oder können nach Beendigung eines Protokoll-Laufs gesundheitsgefährdend werden. Es sollten immer Sicherheitsbrille, zwei Paar Handschuhe und ein Laborkittel getragen werden. Der Betreiber der Anlage ist für die Gewährleistung der Sicherheit am Arbeitsplatz verantwortlich. Er hat sicherzustellen, dass die Bediener des Gerätes ausreichend geschult sind und nicht gesundheitsgefährdenden Konzentrationen toxischer Substanzen (chemischer oder biologischer) ausgesetzt sind, so wie dies in den Sicherheitsdatenblättern oder in anderen zu beachtenden Dokumenten festgelegt ist. Bei der Behandlung von Abluft und bei der Abfallbeseitigung sind alle gesetzlichen Regelungen zur Gesundheit und Sicherheit auf nationaler, regionaler und lokaler Ebene zu berücksichtigen.

* OSHA: Occupational Safety and Health Administration (United States of America).
† ACGIH: American Conference of Government Industrial Hygienists (United States of America).
‡ COSHH: Control of Substances Hazardous to Health (United Kingdom).

WARNING	**Feuergefahr** [W8] Beim Reinigen des QIAxcel Advanced mit einem auf Alkohol basierenden Desinfektionsmittel muss die Tür des QIAxcel Advanced offen gelassen werden, damit die brennbaren Dämpfe entweichen können.

Entsorgen von Abfällen

Benutzte Verbrauchsartikel und Behälter könnten gefährliche Chemikalien enthalten. Derartige Abfälle müssen gesammelt und gemäß den geltenden kommunalen Sicherheitsbestimmungen entsorgt werden.

Weitere Informationen zur Entsorgung vom QIAxcel Advanced finden Sie im Anhang A („Appendix A").

Gefahren durch mechanische Teile

Die Klappen für den Proben- und Cartridge-Einsatz des QIAxcel Advanced müssen während des Betriebs geschlossen sein.

WARNING	**Bewegliche Geräteteile** [W9] Um jeglichen Kontakt mit beweglichen Geräteteilen während des Laufes zu vermeiden, darf der QIAxcel Advanced nur benutzt werden, wenn die Klappen für den Proben- und Cartridge-Einsatz geschlossen sind. Sollten die Sensoren nicht ordnungsgemäß funktionieren, kontaktieren Sie bitten den Technischen Service von QIAGEN.

Symbole auf dem QIAxcel Advanced

Symbol	Fundstelle	Beschreibung
	Plakette auf der Rückseite des Gerätes	CE-Zeichen
	Plakette auf der Rückseite des Gerätes	CSA-Zeichen für Kanada und die USA
	Plakette auf der Rückseite des Gerätes	Hersteller i.S.d. Gesetzes
	Plakette auf der Rückseite des Gerätes	WEEE-Zeichen
	Plakette auf der Rückseite des Gerätes	FCC Markierung der Federal Communications Kommission der USA

10.8 Appendix H

Microsoft Public License

The DotNetZip library is licensed under the Microsoft Public License. See DotNetZipLicense.txt for details.

LibSVM License

QIAxcel ScreenGel uses the LibSVM which is licensed under the following copyright:

Copyright (c) 2000-2012 Chih-Chung Chang and Chih-Jen Lin
All rights reserved.

Redistribution and use in source and binary forms, with or without modification, are permitted provided that the following conditions are met:

1. Redistributions of source code must retain the above copyright notice, this list of conditions and the following disclaimer.

2. Redistributions in binary form must reproduce the above copyright notice, this list of conditions and the following disclaimer in the documentation and/or other materials provided with the distribution.

3. Neither name of copyright holders nor the names of its contributors may be used to endorse or promote products derived from this software without specific prior written permission.

THIS SOFTWARE IS PROVIDED BY THE COPYRIGHT HOLDERS AND CONTRIBUTORS ``AS IS'' AND ANY EXPRESS OR IMPLIED WARRANTIES, INCLUDING, BUT NOT LIMITED TO, THE IMPLIED WARRANTIES OF MERCHANTABILITY AND FITNESS FOR A PARTICULAR PURPOSE ARE DISCLAIMED. IN NO EVENT SHALL THE REGENTS OR CONTRIBUTORS BE LIABLE FOR ANY DIRECT, INDIRECT, INCIDENTAL, SPECIAL, EXEMPLARY, OR CONSEQUENTIAL DAMAGES (INCLUDING, BUT NOT LIMITED TO, PROCUREMENT OF SUBSTITUTE GOODS OR SERVICES; LOSS OF USE, DATA, OR PROFITS; OR BUSINESS INTERRUPTION) HOWEVER CAUSED AND ON ANY THEORY OF LIABILITY, WHETHER IN CONTRACT, STRICT LIABILITY, OR TORT (INCLUDING NEGLIGENCE OR OTHERWISE) ARISING IN ANY WAY OUT OF THE USE OF THIS SOFTWARE, EVEN IF ADVISED OF THE POSSIBILITY OF SUCH DAMAGE.

www.qiagen.com

Australia ■ techservice-au@qiagen.com

Austria ■ techservice-at@qiagen.com

Belgium ■ techservice-bnl@qiagen.com

Brazil ■ suportetecnico.brasil@qiagen.com

Canada ■ techservice-ca@qiagen.com

China ■ techservice-cn@qiagen.com

Denmark ■ techservice-nordic@qiagen.com

Finland ■ techservice-nordic@qiagen.com

France ■ techservice-fr@qiagen.com

Germany ■ techservice-de@qiagen.com

Hong Kong ■ techservice-hk@qiagen.com

India ■ techservice-india@qiagen.com

Ireland ■ techservice-uk@qiagen.com

Italy ■ techservice-it@qiagen.com

Japan ■ techservice-jp@qiagen.com

Korea (South) ■ techservice-kr@qiagen.com

Luxembourg ■ techservice-bnl@qiagen.com

Mexico ■ techservice-mx@qiagen.com

The Netherlands ■ techservice-bnl@qiagen.com

Norway ■ techservice-nordic@qiagen.com

Singapore ■ techservice-sg@qiagen.com

Sweden ■ techservice-nordic@qiagen.com

Switzerland ■ techservice-ch@qiagen.com

UK ■ techservice-uk@qiagen.com

USA ■ techservice-us@qiagen.com

1074975 03/2013

Sample & Assay Technologies